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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; mimunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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Lymphoma
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Abr42859
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Aay34304
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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AAW03757
ADA89266
ADA89274
                                                                    ADJ80323
AAB01949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP45310 standard; protein; 249
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2000US-0240816P.
2001US-0276248P.
2001US-0277379P.
2001US-0293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2002 (first entry)
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17-OCT-2000;
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21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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ABP45310;
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 -MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NoLaN08728463-1/runat_04082005_125805_24527/app_query.fasta_1.is-pa_2=1/USPTO_spool_p/NoLaN08728463-1/runat_04082005_125805_24527/app_query.fasta_1.is-pB=A_Geneseq_oFMT=fastan -SUFFIX=rag -MINNATCH=0.1 -LGOPCL=0 -LOOPEXT=0
-UNITS_bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-UNITS_bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRS=NORMAN08728463-1 @CGN 1 1308 @runat 04082005 125805_24527 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG $CORES=0 -WAIT - DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abp45310 Human BLy
Adg96137 Single ch
Abp44982 Human BLy
Adg95809 Single ch
Abp44943 Human BLy
Adg95770 Single ch
Aaw62794 Amino aci
Aay05694 Multiple
Abg78212 Human Fv
Abg91903 Human ant
                                                                             August 4, 2005, 17:55:32; Search time 92.5 Seconds (without alignments) 677.353 Million cell updates/sec
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                                                                                                                                                    GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC
                                                                                                                                                                                                                                                                        4211384
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                        protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
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45 summaries
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ADG96137
ADG95809
ABP44943
ADG95770
AAW62794
AAW62794
ABG705694
ABG705694
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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ON
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E Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWF) super family and induces B cell through and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lugus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABPA3990-ABPA122B represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
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                                                                                                                                            novel antibodies that immunospecifically
                                                             Antibodies against B Lymphocyte Stimulating polypeptides, diagnosis and treatment of cancers and immune disorders.
Hilbert D;
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Conservative:
Mismatches:
Vaughan T,
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                                                                                                              Claim 1; Page 1979-1980; 3148pp; English
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Choi GH,
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20.63%
20.63%
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                                                                                                                                              invention describes
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Barash SC,
                               WPI; 2002-114799/15
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Best Local Similarity:
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 Ruben SM,
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This invention relates to novel antibodies that immunospecifically Dand chromosome 13934 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scPvs) derived, preferably, from the variable chain antibody molecules (scPvs) derived, preferably, from the variable chary fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods present invention, or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders such, these compositions are useful for identifying immune disorders including mysthemia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ADS and proliferative disorders including leukaemia, carcinoma and cativities such as antirheumatic, antialthritic, neuroprotective, antialthammatory, antiasthmatic, antialthritic, neuroprotective, antiantiammatory, antiasthmatic, antialthritic, neuroprotective, antiantiand specification, but was obtained in electronic format the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                          antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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Matches:
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19-DEC-2001; 2001US-0340817P.
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113.10
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                                                                                                                                                                           110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
                                                                                                                                                                                                                                                         130 GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
                                                                                                                                                                                                                                                                                                                            90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel antibodies that immunospecifically bind to by Dympotycyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS
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              SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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2001US-0276248P.
2001US-0277379P.
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16-MAR-2001;
21-MAR-2001;
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and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered with aberrant stages associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (BLDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibody that immunospecifically binds BLyS SeqID 993
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 AGTCAGGATATTAGCAGC 72
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                                                                                                                                                                                                                                                                                                                                       Sequence 250 AA;
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proliferation and differentiation. Specifically, it refers to single chain antibody molecules (GFCFWs) derived, preferably, from the variable hartibody molecules (GFCFWs) derived, preferably, from the variable havy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The fresher invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This antinflammatory, antiasthmatic, antiallergic and cytostatic. This colypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/published pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLys, B lymphocyte stimulator; TNF superfamily, human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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16-WAR-2001; 2001US-0276248P.
21-WAR-2001; 2001US-0293499P.
25-WAY-2001; 2001US-0293499P.
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Best Local Similarity:
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Pred. No.:
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cytostatic, immunosuppressive, immunostimulant, immunomodulatory, or orbiteration and differentiation. The antibodies D cell invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency and fragments of the antibodies described in the method of
                                                                           Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B cell proliferation, differentiation; scrv; myasthenia gravis; untitiple sclerosis; asthma; rheumatoid arthritis; ADS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiarthmatic; antiallergic; cytostatic
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Matches:
Conservative:
Mismatches:
             Vaughan T,
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             GH,
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            Barash SC,
                                              WPI; 2002-114799/15.
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               Ruben SM,
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to C chromosome 1343 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single contain antibody molecules (ecfvs) derived, preferably, from the variable contain antibody molecules (ecfvs) derived, preferably, from the variable contains region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The person invention refers to the use of such antibodies in various methods contains to inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various cutivities such as antirheumatic, antialerspic and cytostatic. This collymphoma to a proliferative disorders including leukaemia, carcinoma and cutivities such as antirheumatic, antialerspic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format of the printed specification, but was obtained in electronic format.
                                                                                                                                                                                                                                                                                                                                                                                                                                      stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibody that immunospecifically binds to a B lymphocyte stimu (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                Hilbert D;
                                                                                                                                                                                                                Vaughan TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 954; 394pp; English.
                                                                                                                                                                                                                Choi GH,
19-DEC-2001; 2001US-0340817P.
                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                   WPI; 2003-505530/47.
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Matches:
Conservative:
Mismatches:
Indels:
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80.77$
76.92$
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NOLAN463-1A.SEQ (1-81) x AAW62794 (1-80)

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Conservative: Mismatches: Indels:

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Alignment Scores:

92.40 74.07\$ 70.37\$ 66.00\$

Percent Similarity: Best Local Similarity:

Query Match: DB:

RESULT

AAW62794; 

Amino

Multiple sclerosis patient CSF B-cell VH region (clone 4d76) Multiple sclerosis, cerebrospinal fluid; CSF; B-cell; heavy chain variable region; VH gene; somatic hypermutation;

19-JUL-1999 (first entry)

AAY05694;

AAY05694 standard; protein; 97 AA.

Human; immunoglobulin; Ig; transgenic; non-human mammal; inactivated endogenous Ig locus; B-cell development; human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene; kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa; production; antibody. GAAATCAATCATGGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCG----- 54 69 acid sequence of a human antibody fragment. NOLAN463-1A.SEQ (1-81) x ADG95770 (1-253) AAW62794 standard; peptide; 80 AA (first entry) 23-SEP-1998 ч 2

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AAW62793-822 represent fragments of human antibodies produced by transgenic Xenomice, created using the method of the invention. The specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin [Ig] locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus comprising a human micro constant region and regulatory and switch sequences, human J-H genes, and human V-H genes and an inserted human kappa light chain Ig locus in germline configuration, the human J-H genes, and human N-H genes and an inserted human kappa light chain Ig locus comprising a human Kappa constant region, J-kappa genes, and human B-cell development in the human Light chain Ig locus in germline configuration, the human I The chain Ig locus including both a selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human ll-8, EGFR or TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha respectively
                                                                                                                                                                                                                                                                                                                                                                    New transgenic non-human mammals - having an inactivated immunoglobulin
locus and a near complete human immunoglobulin locus, used for production
                                                                                                                                                                                                                                                                              Green L;
                                                                                                                                                                                                                                                                              Mendez M,
                                                                                                                                                                                                                                                                              Klapholz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 71; 128pp; English
                                                                                                                                                                                                                                                                              Jakobovits A, Kucherlapati R,
                                                                                                                                      97WO-US023091
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                                                                                                                                                                                                                                                                                                                                                                                                                    of human antibodies.
                                                                                                                                                                                                                                 (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                       WPI; 1998-333314/29.
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  Homo sapiens.
                                             WO9824893-A2.
                                                                                                                                 03-DEC-1997;
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                                                                                        11-JUN-1998.
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from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF becalls were obtained from 4 MS patients (see AAX5316-19). Differences in nucleotide and predicted amino acid (see AAX05591-94) sequences were compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded eclls from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that havd undergone antigen selection. This finding implicates an important pathogenic pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a heavy chain variable region (VH) as predicted
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B-cell clonality; RA gene; diagnosis; human.
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/label= CDR1
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97CA-02220245.
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label= CDR2
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|abel= FR2
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/label= FR1
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                      Homo sapiens
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The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, compled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                    Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levanon A;
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, Peretz T;
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                                                                                                                        Sequence 97 AA;
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                                                                                                                                                        Alignment Scores:
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the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymboma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one
                                                                                                                                                                                                                                                                                                                         1 GAPATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                         metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; latkiaemia; inflammatory disease; cardiovascular disease; mycardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
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Levanon A;
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Peretz T,
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Amit B, Kooperman L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG91903 standard; protein; 97 AA.
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29-DEC-2000; 2000US-0258948P.
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Richter T,
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antibody or its binding fragment having a first hypervariable region. The disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, cell-matrix, platelet-matrix, platelet cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet of platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet tumction and diseases caused by sulphated tyrosine-dependent protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG 60
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                         Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing framework sequences between non-human and human antibodies. This sequence represents a human heavy chain variable region gene segment used in the
                              comprising making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibody in comparison to for selection, for humanisation. The method is useful for making a humanised antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for direct comparison of framework sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody library; CD1 region; CD2 region; VH region; VL region; immunoglobulin; CD3 region; TM1 scFv; human.
                  The invention describes a method of making a humanised antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein relating to the invention SEQ ID NO:55.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB75646 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                    creation of humanised antibodies
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 97 AA;
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Highly stable artificial antibody libraries with super-repertory and

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Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                       The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a cDNA library as template for amplifying a fragment containing the CDI and CD2 regions of the VH or VL region of immunoglobulin gene and a fragment containing the CD3 region by PCR, respectively, producing VH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-cell; malignant; immunoglobulin; immunoglobulin variable region; Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma.
tool in
               proteomics and e.g. for diagnosis and treating various diseases
   contamination from unexpressible ones, useful as
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Conservative:
Mismatches:
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                                               Page 101; 108pp; Japanese.
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                                                                                                                                                                                                                                                                Sequence 97 AA;
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                                       malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (ig) variable region from the B cell; (b) detecting the region from the B cell; (b) detecting the region from the B cell; (b) detecting the cell as malignant or normal on the basis of the presence or absence of a glycosylation site, and (c) classifying the cell as a glycosylation of the Ig variable region of the B cell receptor and (l) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor; and (3) screening for substances (S) capable of inhibiting the interaction between lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (S) has cytostatic activity, and can be used in gene therapy, and as a glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the cycemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                               1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                               present invention describes a method for classifying a B-cell as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGP antibody heavy chain variable region VH_4-34.
                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x ADD28104 (1-97)
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          Disclosure; Fig 4; 61pp; English.
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29-MAY-2002; 2002US-0384197P.
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                                                                                                                                                                                                                                                                                       92.40
74.07$
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Best Local Similarity:
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(8); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen blinding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody may be variable region sequence used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
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Matches:
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Indels:
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Example 6; Fig 16a; 135pp; English.
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29-MAY-2002; 2002US-0384197P.
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Example 16; Fig 40a; 135pp; English

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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected antibody acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical properties of an antibody especially the stability, the physico-chemical properties of an antibody especially the stability, useful for treating a patient. The present sequence is an antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
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97 119 10 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 0.00847 92.40 74.07**\$** 70.37**\$** 66.00**\$** Score:
Percent Similarity;
Best Local Similarity:
Query Match:
DB: .. 9

NOLAN463-1A.SEQ (1-81) x ADF10150 (1-97)

1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60 g ò

61 GATATTAGC 69

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|||||| ---IleSer 70 69 Search completed: August 4, 2005, 18:14:24 Job time : 97.5 secs

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Sequence 118, Application US/08545809A

Sequence 118, Application US/08545809A

GENERAL INFORMATION:
APPLICANT: HOTOL
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                               Sequence Sequence Sequence 1
                                                                                                                                                 Sequence Seq
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Sequence 4
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILMS DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELEPAN: 617-542-5070
TELEPAN: 617-542-8906
TELERAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-545-809A-92
US-08-767-128-18
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80.7
80.7
79.4
79.4
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    Command line parameters:

ODDEL=Frame+ n2p.model - DEV=xlp

O=/Ggn2_1/USFTO_spool_p/NoLaN08728463-1/runat_04082005_125807_24557/app_query.fasta_1.5

-0=/Ggn2_1/USFTO_spool_p/NoLaN08728463-1/runat_04082005_125807_24557/app_query.fasta_1.5

-0B=168046_Patents_AA - QFWT=fastan - SUFFIX=rai - MINMAYCH=0.1 - LOOPCL=0

-LOOPEXT=0 - UNITS=bits - STRAT=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15

-MODE=LOCAL - OUTFWT=pco - NORM=ext - HEAPSIZES=500 - MINLEN=0 - MAXLEN=200000000

-USRS=NOLAN08728463-1 @CGN 1 1.66 @runat_04082005_125807_24557 - NCPU=6 - ICPU=3

-NO MMAP - LARGEQUERY - NOR SCORES=0 - WAITT - DSPBLOCK=100 - LONGLOG

-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPOP=10 - XGAPEXT=0.1 - FGAPOP=6

-FGAPEXT=0.1 - YGAPOP=10 - YGAPEXT=0.1 - DELOP=6 - DELEXT=0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118, App
Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 25, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7, App
Appli
Appli
                                                                                                                                      4, 2005, 18:05:28; Search time 23.25 Seconds (without alignments) 520.135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                    GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC 81
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
1: /cgn2_6/ptodatcal/iaa/5A_COMB.pep:*
   /cgn2_6/ptodatcal/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatcal/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodatcal/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodatcal/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodatcal/iaa/PcTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                      - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-545-809A-118
US-08-793-450-4
US-09-203-768A-2
US-08-793-450-8
US-09-372-425A-6
US-09-490-153-25
US-09-490-153-25
US-09-490-153-25
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                             NOLAN463-1A.SEQ
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Match Length
                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                               August
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992.4
992.4
992.4
984.4
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984.4
984.4
985.7
980.7
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Maximum DB
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                                                                                                                                             Run on:
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61 GATATTAGC 69
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US-09-203-768A-2
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Best Local Similarity:
Query Match:
                                                   Percent Similarity:
Best Local Similarity:
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Pred. No.:
 Alignment Scores:
Pred. No.:
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US-08-793-450-8
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                                                                                      Query Match:
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER: EMP COMPATION
MEDIUM TYPE: Floppy disk
COMPUTER: EMP COMPATION:
MEDIUM TYPE: Ploppy disk
COMPUTER: BM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PS 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMANTION:
NAME: OBLON, NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 26,6118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMANTION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMANTION:
TELECOMMUNICATION INFORMANTION:
TELEBRONE TOD-413-2000
                                                                                                                                                          116
119
11
11
6
6
                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRAACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
              SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                                             92.40
74.07$
70.37$
66.00$
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-793-450-4
                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||
88 ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                             61 GATATTAGC 69
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                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                       US-08-545-809A-118
                                                                                                                                            Alignment Scores:
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No.:
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Patent No. 6787638

GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: Of Use
TILE REFERENCE: P-IX 2947
CURRENT APPLICANTON NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LEAGHT 139
TURE OF THE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: CHAABIHT, HASSAM
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
ADD
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Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 8, Application US/08793450 ; Patent No. 6312690
            0.000768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.000802
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74.07$
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74.07$
70.37$
66.00$
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                      US-09-372-425A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPS HIS-
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 703-413-3000
TELEFRAK: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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119
11
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US-09-31Z-4Z3A

Patent No. 6475749

GENERAL INFORMATION:

APPLICANT: Sherie L. Morrison

APPLICANT: Improved Rh Antibody

NUMBER OF SEQUENCES: 11

CORRESPEDUNDENCE ADDRESS:

ADDRESSEE: Oppenheimer Wolff & Donnelly LLP

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 9067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows 98

SOFTWARE: MS Word

CURRENT APPLICATION DATE:

FILING DATE: August 11, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOLAN463-1A.SEQ (1-81) x US-08-793-450-8 (1-472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 472 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.00124
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74.07$
70.37$
66.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-793-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                    22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-372-425A-6
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09025769B
Fatent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-EB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                            429
18
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x US-09-372-425A-6 (1-429)
APPLICATION NUMBER:
TILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELEPHONE: (310) 788-500
TELEPHONE: (310) 788-5100
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Bsq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          0.0055487.40
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66.67$
62.43$
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GATATTAGC 69
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                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity:
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Alignment Scores:
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                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09490070A
; Sequence 25, Application US/09490070A
; Patent No. 6686248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Knappik, Achim
; Hord, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE COIN G. Sandercock, Esq. c/o Heller Ehrman
ADDRESSEE COIN G. Sandercock
; STREET: 1666 K Street, N.W., Suite 300
; CTTV. Washingen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IDAPPY disk
COMPUTER: IDAPPE COMPATION TO STATE CANDON DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, ESQ.
REGISTATION NUMBER: 31,298
REGISTATION NUMBER: 31,298
REGISTATION NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               118
18
1
2
6
0
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 912-2020 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDENNES:
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COMPUTER READABLE FORM:
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70.37$
66.67$
60.29$
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STATE: D.C.
COUNTRY: USA
                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 ---IleSer 70
                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

TELECOMMUNICATION INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: 27,794

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREST: 1231 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION' Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                     118
18
1
2
6
0
                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x US-09-490-070A-25 (1-118)
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 118 amino acids
TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
                                                                                                                                       0.00872
                                                                                                                                                            84.40
70.37%
66.67%
60.29%
                                                                                                                                                                                                                                                                                                                                                                                                                             61 GATATTAGC 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                          Sequence 137, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
15
4
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Matches:
Conservative:
Mismatches:
Indels:
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OPERATING SYSTEM: Windows95
SOFTWARE: FastESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,803A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOLAN463-1A.SEQ (1-81) x US-08-545-809A-137 (1-120)
                                                                                              GAAATCAATCATAGTGGAAGCACCAACTACAACCC
                                                         NOLAN463-1A.SEQ (1-81) x US-09-490-324-25 (1-118)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501
TELECHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELER: 200154
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.0248
81.00
79.17%
62.50%
57.86%
   60.29$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GATATTAGCAGC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-545-809A-137
                                                                                                                                                                                              |||||||
---IleSer 70
                                                                                                                                                                   61 GATATTAGC 69
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                                                                                                                                                                                                                                                             US-08-545-809A-137
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 Query Match:
DB:
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                                                                                                                                                                                    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                         50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim
APPLICANT: Knappik, Peter
Ilag, Vic
Ge, Lining
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1221 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                     118
118
12
6
6
                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US/09/490,324
FILING DATE: 2-3an-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               NOLAN463-1A.SEQ (1-81) x US-09-490-153-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid

STRANDEDNESS: «Unknown»

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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84.40
70.37%
66.67%
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70.37%
66.67%
60.29%
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                                                     Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Alignment Scores:
Pred. No.:
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                                                                                          Query Match
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GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/105,617
PRIOR APPLICATION NUMBER: US 08/105,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-05-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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78
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92 AlaThrTyrTyrCysAlaTrpVal 99
                                            92 AlaThrTyrTyrCysAlaTrpVal 99
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------AGCTGGTTA
                                                                                                                   US-08-466-163B-5; Sequence 5, Application US/08466163B
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-802-096-5; Sequence 5, Application US/09802096; Patent No. 6685939; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 CAGGATATTAGC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.028
80.70
47.92%
37.50%
57.64%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 130
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                                       원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGT----- 57
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18
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER KEALANEL FORMY
COMPUTER TEALANEL FORMY
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
SOFERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
APPLICATION NUMBER: US/08/466,151
FILING DATE: US/08/466,151
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/406163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/40617
APPLICATION NUMBER: 08/406617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07/879495
                                                                                                                                                   APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPENDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x US-08-466-151-5 (1-130)
                                                               S-08-466-151-5
Sequence 5, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 CAGGATATTAGC-----
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TYPE: Amino Acid
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37.50%
57.64%
89 SerValAspThr 92
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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Best Local Similarity:
Query Match:
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended, PILE REFERENCE: P0718P2CJUS
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/892,06860
PRIOR APPLICATION NUMBER: US 07/8794,95
PRIOR PILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
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Length:
Matches:
Conservative:
Mismatches:
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Batent No. 6699472

GENERAL INFORMATION

APPLICANT: Jardieu, Paula M.

APPLICANT: Jardieu, Paula M.

APPLICANT: Jardieu, Paula M.

APPLICANT: Jardieu, Paula M.

PAPLICANT: Jardieu, Paula M.

PAPLICANT: Jardieu, Paula M.

PAPLICANT: Jardieu, Paula M.

TILE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C2US

CURRENT APPLICATION NUMBER: US/09/802,077

FRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR PELING DATE: 1992-06-07

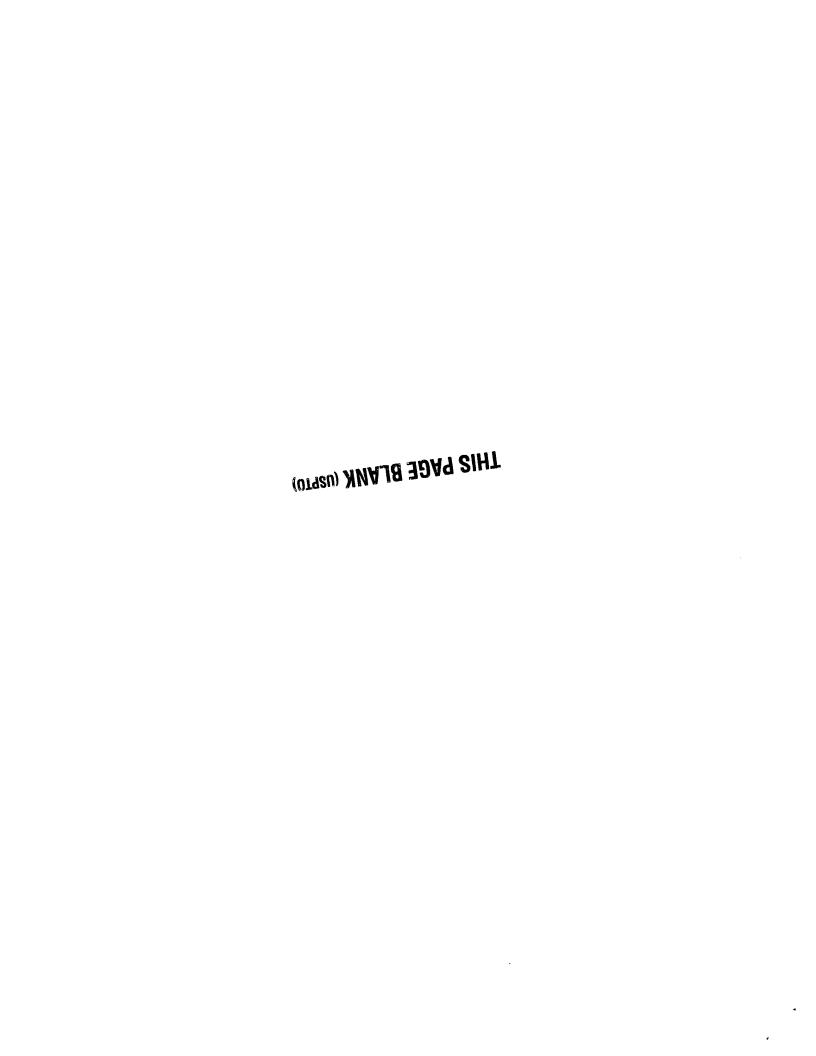
PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGT--
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Matches:
Conservative:
Mismatches:
Indels:
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92 AlaThrTyrTyrCysAlaTrpVal 99
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80.70
47.92%
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 64
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                                         TYPE: PRT
ORGANISM: Mus musculus
US-09-802-096-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-802-077-5
; NUMBER OF SEQ ID NOS:
; SEQ ID NO 5
; LENGTH: 130
                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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Sequence 835, Application US/09471276
; Sequence 835, Application US/09471276
; Retent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dunds Milne Edwards, J.B.
; APPLICANT: Dunds Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: 08/09/471,276
; CURRENT PILING DATE: 1999-12-21
; EARLIER PILING DATE: 1999-12-21
; EARLIER PILING DATE: 1998-04-09
; EARLIER PILING DATE: 1998-04-09
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GlulleAspHisGlyGlyAsnThrAsnTyrAsnProSerLeuLysSerArgVal***--- 95
72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
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Mismatches:
Indels:
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92 AlaThrTyrTyrCysAlaTrpVal 99
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66.67%
59.26%
56.71%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-471-276-835
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LENGTH: 147
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Perfect score:

Sequence:

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Run on:

Scoring table:

Total number

Searched:

Minimum DB Maximum DB

Database

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Sequence 87, Appl
Sequence 47, Appl
Sequence 128, Appl
Sequence 44115, A
Sequence 90, Appl
Sequence 192, Appl
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Sequence 87, P
Sequence 87, P
Sequence 83, P
Sequence 87, P
Sequence 87, P
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Sequence 1321, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 00/240,816

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499
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0.05-09-864-761-44315

0.05-09-864-761-92

0.05-09-910-942-118

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0.05-09-910-675-2

0.05-09-912-656-66

0.05-09-972-656-66

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0.05-09-972-656-82

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0.05-09-810-748-1133

0.05-09-810-748-1133

0.05-09-810-748-118-1659

0.05-09-810-748-118-1
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SUMMARIES
                                                               Length
                                        Query
Match 1
                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
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-DB=Published Applications AA -QFMT=fastan -SUFFTX=rapb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LiST=45 -DOCALIGN=200 -TRR SCORE=pct -THR MAX=100
-THR MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                        4, 2005, 18:20:25; Search time 80.25 Seconds (without alignments) 788.093 Million cell updates/sec
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                                                                                                                                                                                                                                                                                   GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Alignment Scores:
Pred. No.:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/341,469
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-3-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-01-17
PRIOR PILING DATE: 2000-01-17
PRIOR PILING DATE: 2000-06-16
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Matches:
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113.10
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1221
LENGTH: 249
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                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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Sequence 12, Application US/10898408

Sequence 12, Application US/10898408

Publication No. US20050058642A1

GENERAL INFORMATION:

APPLICANT: GALIBERT, Laurent J.

TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE

FILE REFERENCE: 346'-A

CURRENT PILING DATE: 2004-07-23

PRIOR APPLICATION NUMBER: 60/490,027

PRIOR FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 12

LENGTH: 115
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Matches:
Conservative:
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Gaps:
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Matches:
Conservative:
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96.40
41.18%
37.25%
68.86%
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo mapiens
US-10-293-418-1321
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ORGANISM: homo sapiens
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Best Local Similarity:
Query Match:
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Percent Similarity:
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Publication No. US20030059937A1

GENERAL INPORMATON:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATCHTIN VEY: 2.0

LENGTH: 250

LENGTH: 250
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Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT EPLING DATE: 2002-11-27
FRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
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Matches:
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NOLAN463-1A.SEQ (1-81) x US-10-898-408-12 (1-115)
                                                                                                    61 GATATTAGC------
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CORGANISM: Homo sapiens
US-09-880-748-993
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US-10-293-418-993
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iS-09-880-748-954

iS-09-880-748-954

iS-09-880-748-954

iS-09-880-748-954

iGENERAL INFORMATION:

APPLICANT: Ruben et al.

iTILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

iTILE OF INVENTION: PAPLICATION NUMBER: 60/212,210

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2000-10-17

PRIOR PLILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-25

iNUMBER: OF SEQ ID NOS: 3239

iSEQ ID NO 954

iLBNGTH: 253

TWORD: DATE: 2001

iLBNGTH: 253

TWORD: DATE: 2001

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Indels:
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PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-010-17
PRIOR FILING DATE: 2000-10-17
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67.00%
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CORGANISM: Homo sapiens
US-10-293-418-993
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CRGANISM: Homo sapiens
US-09-880-748-954
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Best Local Similarity:
Query Match:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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TITLE OF INVENTION: PLURAL Vh AND VK REGIONS AND ANTIBODIES PRODUCED
TITLE OF INVENTION: THEREPROM
FILE REFERENCE: CELL 4.18 COM
CURRENT APPLICATION NUMBER: US/10/078,958
CURRENT FILING DATE: 1002-02-19
PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 80
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Homo sapiens
US-10-078-958-2
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US-10-194-975-40
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF529P2

CURRENT PELINGE: PF529P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-219

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2000-06-16

PRIOR PILING DATE: 2000-06-16
                                                                           GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCG---
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Matches:
Conservative:
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                                         NOLAN463-1A.SEQ (1-81) x US-09-880-748-954 (1-253)
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US-10-078-958-2; Sequence 2, Application US/10078958; Sequence 2, Application No. US20030070185A1; CENERAL INFORMATION:
APPLICANT: JAKOSOVITS, AYA; APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: MENDEZ, SUSAN; APPLICANT: MENDEZ, MICHAEL J.
APPLICANT: GREEN, LARRY
                                                                                                                                                                                                                                      Sequence 954, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
                                                                                                                                         55 AGTCAGGATATTAGCAGC 72
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70 SerGlnAspThrSerAsn 75
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/46
CURRENT FILING DATE: 2001-12-31
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PASESEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES, AND USES THEREOF TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REPERROCE: 10793/45 CURRENT APPLICATION NUMBER: US/10/032,423A CURRENT FILING DATE: 2001-12-31 PRIOR APPLICATION NUMBER: 60/258,948 PRIOR PILING DATE: 12/29/2000 NUMBER OF SEQ ID NOS: 204 SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                    ; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
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LENGTH: 97
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Sequence 87, Application US/20040001822A1

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT PILING DATE: 2001-12-31

PRIOR PILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SEQ ID NO 87

LENGTH: 97
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US-10-308-817-83

Sequence 83, Application US/10308817

Publication No. US200319861A1

GENERAL INFORMATION:

APPLICANT: Rother, Russell

APPLICANT: Wu, Dayang

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 1087-37

CURRENT PILING DATE: 2002-12-03

NUMBER OF SEQ ID NOS: 195

SOFTWARE: Patentin version 3.1

SEQ ID NO 83

LENGTH: 97
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ORGANISM: human
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US-10-032-037B-87
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Fublication No. US20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY.
TITLE OF INVENTION:
TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR PILING DATE: 12/29/2000
PRIOR FILING DATE: 12/29/2000
SPINGRED FEED TO NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
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                                                                                                                 ; Sequence 83, Application US/10453698; Publication No. US20040038308A1; Publication No. US20040038308A1; APPLICANT: Rother, Russell; TLLE OF INVENTION: HYBRID ANTIBODIES; FILE REFERENCE: 82 CIP (1087-37 CIP); CURRENT APPLICATION NUMBER: US/10/453,698; CURRENT FILING DATE: 2003-06-03; NUMBER OF SEQ ID NOS: 196; SOFTWARE: Patentin version 3.2; SEQ ID NO 83
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ORGANISM: Homo sapiens
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Query Match:
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; ORGANISM: human
US-10-453-698-83
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US-10-029-926B-87
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US-10-029-926B-87
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US-10-453-698-83
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
R;Mang, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Reference preliminary
A;Rolecule type: DNA
A;Residues: 1-97 WENA
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Ig heavy chain V region - human
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      61 GATATTAGCAGC
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-MODEL=frame+ n2p.model -DEV=xlp
-G-/cgn2 1/USFTO-gpool p/NOLAN08728463-1/runat_04082005_125806_24544/app_query.fasta_1.5-g-/cgn2 1/USFTO-gpool_p/NOLAN08728463-1/runat_04082005_125806_24544/app_query.fasta_1.5-DSE=PIR -QFRT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LCOPCL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=DO -TRE NINLEN - MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1 1 77 @runat_04082005_125806_24544 -NCPU=6 -ICFU=3
-UNITS-DO MAND -LARGEGUERY -LEAS SCORES=0 -MATT -DSPBLOCK=100 -LONGIAG
-DRO MAND -LARGEGUERY -LEAS SCORES=0 -MATT -DSPBLOCK=100 -LONGIAG
-DRO MAND -LARGEGUERY -LG SCORES=0 -MATT -DSPBLOCK=100 -LONGIAG
-DRO TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -YGAPOP=6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
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1 GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                            protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 200000000
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2: pir2:*
3: pir3:*
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Database

111110987654321

Result No.

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C.Species: Homo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C.Date: 106-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C.Paccession: 837454
R.McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A.Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from p
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S;8805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Rur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376 C.Superfamily: immunoglobulin V reggion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;Keywords: heterotetramer; immunoglobulin F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                     A; Experimental source: V(H)4.2
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < LNM>
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A;Status: translation not shown
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                                                                  A, Cross-references: EMBL: X56364
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66.00$
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Best Local Similarity:
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A,Molecule type: DNA
A,Residues: 1-97 <WEN>
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Best Local Similarity:
                     A; Molecule type: DNA
A; Residues: 1-97 <SAN>
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Pred. No.:
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Histinfranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.B.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
C;Accession: S26898; S12420
B;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; WUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
A; Experimental source: clone DP-63
R; Sanz. 1.; Kelly, P:; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741.3748, 1989
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; MUID:90059975; PMID:2511001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 AlaAspThrAlaValTyrTyrCysAlaArgGlyGlySerValLeuArgPheLeuGluTrp 121
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                  Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Homov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78052; S23717 R;Harindranath, N.
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 15-111 < HAW>
A; Cross-references: EMBL:X54441
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin (fragment) #status predicted <SIG>
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>
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21
241
141
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Matches:
Conservative:
Mismatches:
                                                                                                                                    submitted to the EMBL Data Library, August 1990
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A; Residues: 1-140 <HAR>
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A,Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin A;Reference number: 847010
A;Accession: 847010
A;Accession: 847010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Residues: 1-126 <MAH>
CONSEreferences: BMBL:235492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < NMM>
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C;Accession: PS0341
B;Chem. Biophys. Res. Commun. 182, 1260-1263, 1992
A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell A;Reference number: PS0341; MUID:92171937; PMID:1540170
A;Molecule type: mRNA
A;Residues: 1-133 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-38/Region: framework 1
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C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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F;44-57/Region: framework 2
F;58-74/Region: complementarity-determining
F;75-106/Region: framework 3
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E. submitted to the EMBL Data Library, July 1994
A;Reference number: S37453
A;Accession: S37454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>A;Residues: 1-106 <MCI>C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Or-Sep-1990 #sequence_revision O7-Sep-1990 #text_change O9-Jul-2004
Cispacesion: G34964
Risanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1389
A,Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals apientitle: Nucleotide sequences of eight human natural autoantibody V-H regions reveals apientitle: Nucleotide sequences of eight human natural autoantibody V-H regions reveals apienties and the sequences of eight human natural autoantibody V-H regions reveals apienties and the sequences in NIPROT: Q8WUX4; GB: M26998
A,Cross-references: UNIPROT: Q8WUX4; GB: M26998
C; Superfamily: immunoglobulin V region; immunoglobulin homology < IMM>
F;15-97/Domain: immunoglobulin homology < IMM>
                                B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATCAATGATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG
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R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, A;Reference number: A23746; WUID:91131575; PMID:1993660
                                                                                                                                                                                                                                                                         A;Molecule type: procein
A;Residues: 1-231 <LEO.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V-IV region (Ab44) - human
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B49028
Ig heavy chain V-IV region - human (fragment)
C;5pecies: Home saptens (man)
C;5pecies: Trimmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur Bur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Reference number: A49028
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 < TINA
A;Residues: 1-143 < TINA
A;Residues: 1-143 < TINA
A;Residues: L-143 < TINA
A;Residues: L-143 < TINA
A;Residues: L-143 < TINA
A;Residues: Reguence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A;Reference number: A49045, MUID:92324290; PMID:1623923
A;Accession: A49045
A;Satus: preliminary
A;Satus: preliminary
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A; Residues: 1-140 <GRI>
A; Residues: 1-140 <GRI>
A; Residues: 1-140 <GRI>
A; Residues: 1-140 <GRI>
A; Cross-references: GB:S39381; NID:9250899; PIDN:AAB22441.1; PID:9250900
A; Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-116 / Domain: immunoglobulin homology <IMM>
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C;Accession: S44114

R;Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the BMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
                                                                                                                                                                                                                 Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
                                 50 GlullelleHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 4, 2005, 18:21:23
Job time : 20.25 secs
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81.40
67.86%
60.71%
58.14%
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                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: $44105
A;Accession: $44114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAM>
                                                                                           69
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                                                                                           GATATTAGC
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Best Local Similarity:
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                                                                                           61
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S14474

S14474

Ig heavy chain V region - human

C;Species: Home sapiens (man)

C;Species: Home sapiens (man)

C;Species: Home sapiens (man)

C;Species: Home sapiens (man)

C;Accession: S14474

R;Van Bs. J.H.; Gamelign Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H.

Submitted to the EMBL Data Library, November 1990

A;Reference number: S14474

A;Accession: S14474

A;Accession: S14474

A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X56591; NID:G37235; PIDN:CAA39929.1; PID:g1335354

C;Superfeamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <IMM>
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
C;Accession: S26905; S12419
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905
A;Status: preliminary
                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-98 < TOM>
A; Cross Sereferences: EMBL: 212370; NID: g32960; PIDN: CAA78240.1; PID: g32961
A; Cross Serignated DP-70
R; Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
R; Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; WID: 90059975; PMID: 2511001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 69
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                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-98 «SAN»
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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84.40
70.37%
66.67%
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83.40
70.37$
66.67$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
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Best Local Similarity:
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homo sapien
homo sapien
caenorhabdi
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mus musculu
oceanobacil
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corynebacte
homo sapien
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bacillus th
bacillus ce
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arabidopsis
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listeria in
                                                                                                                                                                                                                                                                                                                                      arabidopsis
                                       mus musculu
                                                                                            saccharomyc
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                                                                                                                                                                                                                                                        homo sapien
                                                                                                                                                                                                                                                                  moorella th
picrophilus
                                                                                                                                                                                                                                                                                                                        rhizobium m
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                                                                                                                                                                                                                               nonomuraea
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TISSUE-Hodgkin lymphoma;
Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Submitted (MAY-2013) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ564425; CAD92032.1; -.
HSSP; P18532; IKCV.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM0406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
         QBZ 027
QG mx1
QG myh3
QC 175 379
QC 175 379
QC 175 379
QC 1822
QC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE3D8A846616C908 CRC64;
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119
119
0
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rearranged VH4-34 V gene segment (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA
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                                                Q6NYH3
Q7Z379
O17575
TFC3 YEAST
O95973
Q9FL48
                                                                                                                                Gelbos
HV46 MOUSE
UPP OCEIH
Q8XWU0
                                                                                                                                                                                  Q6NGD8
DPO4_CORGL
KG88_HUMAN
Q7WZ77
                                                                                                                                                                                                                                       OBP5M2
O96KX8
DCMA_MOOTH
Q6L0H3
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YBX0_ARATH
Q6HH<del>6</del>0
                         Q6GMX1
HV60 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                             09VKG8
0926K5
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Q813F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOLAN463-1A.SEQ (1-81) \times Q7Z3Y6 (1-116)
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74.07$
70.37$
66.00$
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                                                                                                                                                                                                             1083
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337
1916
212
360
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Best Local Similarity:
                                                                                                                                                                        39.3
39.3
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40.9
38.3
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Pred. No.:
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57.8
57.5
57.5
4.75
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59.5
59.4
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NON TER
SEQUENCE
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Q7Z3Y6
Score:
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                                                                                       4, 2005, 17:55:57; Search time 83.75 Seconds
(without alignments)
990.529 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo
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1 GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC
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QGgmx5
Q9bu10
Q9bqba
Q9bqba
Q6pqi8
Q6gmx7
Q6gmx7
Q99m22
Q99m22
Q96ey0
Q66ey0
Q96ey0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07z3y6
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                              protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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                                                                                                                                              NOLAN463-1A.SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                          August
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Match
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69.3
69.1
                                                                                                                                                         Perfect score:
                                                                                                                                                                                                Scoring table:
                                                              OM nucleic -
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No.
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N

69

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61 GATATTAGC
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                                                                                     RESULT 3
                                                                                                        26GMX5
                                                                                                                                    셤
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toodhiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones C.J., Marra M.A.,
Jones S.J., Marra M.A.,
Jones G.J., Marra M.A.,
Johns S.J., Marra M.A.,
Johns J. Marra M.A.,
Johns S.J., Marra M.A.,
J
                    68
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AM19235.2; -.
PIR; (34964, 134964.
HSPP; P01861; 1ADQ.
Pfam; PP07654; C1-set; 4.
SMART; SM00409; IG: 2.
SMART; SM00407; IGc1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .l protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
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119
119
0
                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                        Created)
                                                                                                                                                       PRT;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.40
74.07%
70.37%
66.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                     Q8WUX4;
01-MAR-2002 (TrEMBLrel.
                                                    69
                                                                                   ---IleSer 70
                                                                                                                                                                                                                                     Hypothetical protein. Homo sapiens (Human).
                                                    GATATTAGC
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue=Lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                   20
                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                     Q8WUX4
                                                                                                                    RESULT 2
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TISSUELY FROM N.A.

TISSUELYMPH;

TISSUELYMP
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073767; AAH73767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65304 MW; 2A1E75F6AED85230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                              597 AA.
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                               Created)
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR003597; Ig. c1.
InterPro; IPR003606; Ig. MHC.
InterPro; IPR003596; Ig. v.
Pfam; PP00467; C1-set; 4.
Pfam; PP00407; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGc1; 4.
                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.00427
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74.07$
70.37$
66.00$
                                                                                                                                                  PRELIMINARY;
96
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SEQUENCE 597 AA; 6
   ---IleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
   95
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG

NOLAN463-1A.SEQ (1-81) x Q6GMX5 (1-597)

ò

1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGGTCCCTCAAGAGTGGGGGGAGTCAG 60

IGHM protein. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[1] SEQUENCE FROM N.A.

NCBI\_TaxID=9606;

01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

625 AA.

PRT;

PRELIMINARY;

Q96AA6; **096AA6** 

RESULT 5

69

61

---ileser 89 GATATTAGC

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Trausbes-Tympho.

NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

L. Artschul S.P., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwam P.J., McKernan K.J., Malek J.A., Gunstanne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rachylor, Helton B., Ketteman M., Madan A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Norley W., Marra M.A.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
                   87
01-JUN'2001 (TrEMBLrel. 17, Created)
01-JUN'2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
IGHM protein.
Hamo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; Prv.oss., 1Gv; 1.
SMART; SW00406; 1Gv; 1.
PROSITE; PS00290; 1G_MHC; UNKNOWN 3.
PROSITE; PS07 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
119
66
66
66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                    597 AA
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig WHC.
Pfam; PF07654; Cl-set; 4.
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74.07$
70.37$
66.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                    PRELIMINARY;
                                                  61 GATATTAGC 69
                                                                                ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                   .69
                                                                                  88
                                                                                                                                                                        Q9BU10;
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                                                                                                                                   Score:
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TISSUE-Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WETAUSDERG R.L., Feligood B.A., Grouse L.H., Schaefer C.P., Bhat N.K.,

Altschul S.F., Zeeberg B., Buedrow K.H., Schaefer C.P., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Distribution M.J., Garres M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.2; -.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 625 AA; 68610 MW; P62FAB3ADE7ECBFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625
119
119
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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InterPro; IPR003109; Ig-11ke.
InterPro; IPR003101; Ig-21.
InterPro; IPR003606; Ig_MHC.
InterPro; IPR003606; Ig_V.
Pfam; PP07654; C1-8et; 4.
SMART; SM00407; IG21; 4.
SMART; SM00407; IG21; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.40
74.07$
70.37$
66.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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NOLAN463-1A.SEQ (1-81) x Q96AA6 (1-625)

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NOLAN463-1A.SEQ (1-81) x Q9BU10 (1-597)

g

Best Local Similarity:

Query Match: DB:

Percent Similarity:

1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60

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RESULT 7
                                                                           셤
                                                                                                                                                                                                                                                                                  A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Mang J., Haich F.,

Rapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldon M.F., Caraninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Ale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schwerchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Corse S.J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO06180; AAH06180.1; -.
HSSP; P01061; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART, SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SEQUENCE 597 Aa; 65300 MW; 2DĀRAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597
118
22
6
                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                597 AA
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOLAN463-1A.SEQ (1-81) x Q9BQB8 (1-597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig cl.
Interpro; IPR003066; Ig MHC.
Interpro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; dy v.
                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0281
86.40
70.37%
66.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
                                                                                                                PRELIMINARY;
                                      69
                                                            ---IleSer 96
                                                                                                                                                                                       Homo sapiens (Human)
                                      GATATTAGC
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissum=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                69BQB8
                                                                                                                                                                            IGHM
                                                                                        RESULT 6
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TISSUB-Primary B-Cells,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MALA Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jedach H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,

Braheton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milaton M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Mark M. Madan A., Young M. M., Madan A., Schnerch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Redeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576
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Last annotation update)
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Conservative:
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Indels:
Gaps:
                                                                                                                                                                          576 AA.
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                                                                                                                                                                                                                                   Created)
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, POUSDES, 1AAN.
InterPro; IPR003599; Ig.,
InterPro; IPR003599; Ig.,
InterPro; IPR003597; Ig.,
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WC.
Pfam; PP07654; Cl-set; Z.
Pfam; PP07654; Cl-set; Z.
Pfam; PR00407; ig; 1.
SMART; SM00407; IG:1; 3.
SMART; SM00407; IGC1; 3.
                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC063384; AAH63384.1;
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70.37%
66.67%
60.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Primary B-Cells;
69
                                                        89
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
  61 GATATTAGC
                                                     ---Ileser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                   IGHD protein.
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                                                                                                                                                                                                        Q6P4I8;
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                                                                                                                                                                    Q6P4I8
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NOLAN463-1A.SEQ (1-81) x Q6P4I8 (1-576)

69

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NOLAN463-1A.SEQ (1-81) x Q6GMX7 (1-477)
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                                                                         64 ATT-----
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---IleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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SEQÜENCE
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Batchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., McKernan K.J., Mbramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nollalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. "Generation and initial analysis of more than 15,000 full-length human
            GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                               Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 51631 MW; 9FE59C09C50CFF85 CRC64;
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33
44
127
                                                                                                                                            05-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                        477 AA
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 477 AA; 51631 MM; 9FE59
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC073765; AAH73765.1; ...
InterPro; IPR0031599; Ig.
InterPro; IPR003109; Ig.-like.
InterPro; IPR003597; Ig.cl.,
InterPro; IPR033596; Ig_WHC.
Pfam; PR07654; Cl-8et; Z.
Pfam; PF00477; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.135
81.30
39.22%
33.33%
58.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00409; IG; 4.
SM00407; IGc1; 3
SM00406; IGv; 1.
                                                 69
                                                                       ---IleSer 97
                                             GATATTAGC
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local Similarity;
Query Match:
DB:
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Pred. No.:
                                                 61
                                                                                                                        Q6GMX7
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90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109
99 ---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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V segment.
D segment.
J segment.
By similarity.
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                    -----AGCAGCTGG 75
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-II region ARH-77 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1. SMART; SM00406; IGV; 1. SMOSTTE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal. SIGNAL.
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78.40
66.67$
62.96$
56.00$
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PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOLAN463-1A.SEQ (1-81) x Q99M22 (1-479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR0030596; Ig_MHC.
Pfam; PF07654; Cl_set; Z.
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                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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72.60
33.93%
30.36%
51.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OOG BACOOC BACOO
      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 ValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YN19 of B cells (Ramos cell line)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CAGGATATTAGCAGC
                                                                                                                                                                                                                                                                                                                                                                             TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX248300; CAD62627.1; -.
HSSP; P01820; IGJJ.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SM00406; IGv; 1.
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
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139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOLAN463-1A.SEQ (1-81) x Q86SX2 (1-139)
                                                                                                                                                                            Homo sapiens (human) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 139 AA; 15573 MW;
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73.70
35.71%
30.36%
52.64%
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PRELIMINARY;
                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=B cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells;
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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DB:
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                           Q86SX2
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099M22
AC 099M2
DT 01-JU
DT 0
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90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrThrGluAspThr 109
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brada S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko Y., Boutfard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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TISSUB-Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingoolf E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
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22
34
134
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=mix FVB/N; TISSUE=Mammary tumor; Strausberg R.;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Latchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Halton E., Ketreman M., Madan A.M., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAGGATATTAGCAGC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
1GHM protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
REMBL, BC073766; AAH73766.1; -.
InterPro; IPR003599; Ig. 1.
InterPro; IPR003599; Ig. 2.
InterPro; IPR003597; Ig. 2.
InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig W.
Refam; PF07654; C1-set; 3.
Refam; PF07654; C1-set; 3.
Refam; PR00409; Ig. 4.
SMART; SM00409; IG.; 2.
SMART; SM00406; IGC1; 3.
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13
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Matches:
Conservative:
Mismatches:
Indels:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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80.00%
65.00%
51.43%
                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 465 AA; 5
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Best Local Similarity:
Query Match:
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Pred. No.:
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Q96EY0
       셤
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Sacres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A., Faheton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

TISSUB-Hybridoma;
MEDLINE=96211469; bubMed=8648670;
Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
"Targeting human immunodeficiency virus type 1 reverse transcriptase by intracellular expression of single-chain variable fragments to inhibit early stages of the viral life cycle.";
EMBL, U48716; AAB64342.1; -.
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25-OCT_2004 (TrEMBLrel. 28, Last sequence update)
25-OCT_2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, PO1820; JG7J.

InterPro; IPR003599; Ig.

InterPro; IPR0031006; Ig_like.

InterPro; IPR0031006; Ig_MHC.

InterPro; IPR003596; Ig_W.

InterPro; IPR003596; Ig_W.

InterPro; IPR003596; Ig_W.

InterPro; IPR003596; Ig_W.

InterPro; IPR00409; IG_-eet; 4.

INTERPRO; IPR00409; IG 2.

INTERPRO; IRR JEC-like.

INTERPRO; IPR00409; IG_WHC; UNKNOWN 3.

INTERPRO; IRR JEC-like; 5.

INTERPRO; IRR JEC-like; 5.

INTERPRO; INTER; PS00290; IG_WHC; UNKNOWN 3.

INTERPRO; INTER; PS00290; IG_WHC; UNKNOWN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.2; -.
PIR; S15590; S15590.
HSSP; P01820; 1G7J.
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cal Similarity:
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Q65ZI1
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

InterPro; IPR001599; Ig.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR001596; Ig_v.

R Pfan; PF00047; ig; 2.

R NART; SM00408; IGc2, 2.

R SMART; SM00408; IGc2, 2.

R SMART; SM00408; IGc2, 2.

R RNART; SM00408; IGv. 2.
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MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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13219 MW; 1BDB86B6420EA0BE CRC64;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF033041; AAD56277.1; -.
PIR; PH0876; PH0876.
PIR; S12416; S12416.
HSSP; P01820; 1G70.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGV; 1.
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119 AA;
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Search completed: August 4, 2005, 18:20:06 Job time : 89.75 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - protein search, using frame plus n2p model	Run on: August 4, 2005, 17:55:32 ; Search time 92.5 Seconds (without alignments) 677.353 Million cell updates/sec	Title: NOLAN463-1B.SEQ Perfect score: 140 Sequence: 1 CGGGCGAGTCAGGATATTAGACAACCCGTCCCTCAAGAGT 81	Scoring table: BLOSUM62  Xgapop 10.0 , Xgapext 0.1  Ygapop 10.0 , Ygapext 0.1  Fgapop 6.0 , Fgapext 0.1  Delop 6.0 , Delext 0.1	Searched: 2105692 seqs, 386760381 residues	Total number of hits satisfying chosen parameters: 4211384	Minimum DB seg length: 0 Maximum DB seg length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters:  -MODEL=frame+ n2p.model -DEV=xlp -Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125805_24527/app_query.fasta_1.5 -DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LÖOPCL=0 -LOOPEXT=0 -UNITS=blats s-STAFT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LISE-45 -DOCALICAN-200_mup_const_c	-OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLENS -MAXLENS=200000000 -UBER=NOLANO8728463-1 @CGN 11 308 @runat 04082005 125805 24527 -NCPU=6 -ICPU=3 -NO MMAP -LARGENGERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGIAG -DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP-0 -XGAPEXT=0.1 -FGAPOP=6 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1			1: geneeqp2002s:* 6: genesqp2003as:* 7: genesqp2003bs:* 8: genesqp2004s:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Query Match Ler		98.2 70.1 97 5 ABG91903 98.2 70.1 97 6 ABO27107 98.2 70.1 97 7 ADB75646 98.2 70.1 97 7 ADD28104

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Exemplocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell tumour and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant ENS expression and activity of autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency (GVID) and the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                         This invention describes novel antibodies that immunospecifically bind to
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                                                                   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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 Vaughan T, Hilbert D;
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Choi GH,
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 Ruben SM,
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to Ciromosome 1943 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrws) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The resent invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This antiinflammatory, antiasthmatic, antiallergic and cytostatic. This antiinflammatory, antiasthmatic, antiallergic and cytostatic. This circumic format of nor form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                        Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                  Choi GH,
14-NOV-2002; 2002WO-US036496.
                                    16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                  Ruben SM, Barash SC,
                                                                                                                                                                      WPI; 2003-505530/47.
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The present invention describes a protein comprising an immunoglobulin (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL) addomain. The protein binds a complex comprising a major histocompatibility complex (MHC) and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide comprising the novel protein and a carrier; (2) a cytotoxic T cell comprising one or more nucleic acids for expressing the Ig that binds a comprising one or more nucleic acids for expressing the Ig that binds a comprising one or more nucleic acids for expressing the Ig that binds a comprising one or more nucleic acids for expressing the Ig that bind the UC comprising an MHC and a peptide, and does not substantially bind the MHC in the absence of the MHC; (3) an isolated nucleic acid acid sequences that encodes the comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the protein; (5) a transgenic animal whose genome includes heterologus concern; (5) a transgenic animal whose genome includes heterologus concern that specifically binds the MHC-peptide complex; (7) expressing a cancerous disorder in a subject; and (10) detecting an MHC-peptide complex in a sample. A protein of the invention has cytostatic activity, and composition for treating or preventing a composition for peptide complex in a supject of an antibody which binds to an MHC-peptide complex in the peptide component in as peptide on a peptide component of peptide complex where the peptide component in a supject of an antibody which binds to an MHC-peptide complex where the peptide component in a supject of an antibody which binds to an MHC-peptide complex where the peptide component in a supject of an antibody where the peptide or an 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
                   immunoglobulin; Ig; heavy chain variable domain;
light chain variable domain; major histocompatibility complex; MHC;
gpl00; MUCl; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 28B; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DYAX-) DYAX CORP.
(TECR ) TECHNION RES & DEV FOUND
                                                                                                                                                                                                                                                                                                                                            20-FEB-2003; 2003WO-US005128.
                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2002; 2002US-0358994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoogenboom HRJM, Reiter Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-663847/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADA89273.
                                                                                                                                                                                                                                      WO2003070752-A2.
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                        28-AUG-2003
                                                                                                                                                       Synthetic
                                                                                                        cancer.
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Sequence 125 AA;

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125
122
22
22
121
       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
       000565
              99.90
50.00%
47.83%
71.36%
                                 Best Local Similarity:
                        Percent Similarity:
Alignment Scores:
                                        Query Match:
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NOLAN463-1B.SEQ (1-81) x ADA89274 (1-125)

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26 GlyGlySer----IleSerSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44
3 GGCGAGTCAGGATATTAGCAGC-----
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Human, immunoglobulin, Ig, transgenic, non-human mammal, inactivated endogenous Ig locus; B-cell development, human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene; kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa; production; antibody. 7 64 44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe Mendez M, Amino acid sequence of a human antibody fragment. Klapholz S, AAW62794 standard; peptide; 80 AA. Kucherlapati R, 97WO-US023091. 96US-00759620. (first entry) 81 67 (ABGE-) ABGENIX INC. WPI; 1998-333314/29. CCTCAAGAGT Jakobovits A, Homo sapiens. 03-DEC-1996; 03-DEC-1997; MO9824893-A2 23-SEP-1998 11-JUN-1998. AAW62794; 25 72 AAW62794 RESULT 원 셤 ठ

New transgenic non-human mammals - having an inactivated immunoglobulin locus and a near complete human immunoglobulin locus, used for production of human antibodies.

Disclosure; Page 71; 128pp; English.

transgenic Xenomice, created using the method of the invention. The profitation describes a transgenic non-human mammal which has genome specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin (Ig) locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in micro constant region and regulatory and switch sequences, human J-H genes, and human V-H genes and an inserted human kappa light chain Ig locus in germline configuration, the human J-H genes, where the number of V-H and v-kappa genes, inserted are selected to restore normal B-cell development in the mammal. The selected to restore normal B-cell development in the mammal. The call cours channed have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human IL-B, EGFR or TNF- alpha the mice will produce antibodies to IL-B, EGFR or TNF- alpha respectively

Sequence 80

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80
19
3
        Length:
Matches:
Conservative:
Mismatches:
       0.000842
98.20
65.62%
59.38%
                                   Best Local Similarity:
                         Percent Similarity:
Alignment Scores:
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19-SEP-1997;
04-NOV-1997;
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                                        Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
                                                                                                                                                      Multiple sclerosis; cerebrospinal fluid; CSF; B-cell; heavy chain variable region; VH gene; somatic hypermutation; B-cell clonality; RA gene; diagnosis; human.
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                                                                                                                                                                                                                                       'note= "replaces Glu of RA"
                                                                                                                                                                                                                                                                'note= "replaces Gly of RA"
                                                                                                                                                                                                                                                                              note= "replaces Phe of RA"
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Indels:
Gaps:
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                    NOLAN463-1B.SEQ (1-81) x AAW62794 (1-80)
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                                                           ACAACCCGTCCCTCAAGAGT 81
                                                                  AAY05694 standard; protein; 97
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/label= CDR2
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                                                                                                                                                                                                                                                                                                 1. .36
label= CDR1
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|abel= FR2
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/label= FR1
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                                                                                                                             (first entry)
70.14%
2
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                                                                                                                                                                                  Homo sapiens
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                                                                                                                             19-JUL-1999
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Region
Query Match:
DB:
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This sequence represents a heavy chain variable region (VH) as predicted from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal from DNA of a multiple sclerosis (MS) patient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19). Differences in nucleotide and predicted amino acid (see AAX05691-94) sequences were compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded B-cells from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that havd undergone antigen antibody-forming or memory lymphocytes that havd undergone antigen the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determination of B-cell clonality by amplification or enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Fv molecule hypervariable region related peptide #87.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9D; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG78212 standard; protein; 97 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-2001; 2001WO-US049440.
97CA-02216595.
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98.20
65.62$
59.38$
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                                                                                                                                                                   WPI; 1999-276985/23.
N-PSDB; AAX25318.
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                                                                       (QINY/) QIN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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nolan463-1b.seq.rag

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11-JUL-2002.
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IID ABO2
XX
AC ABO2
XX
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DT 10-6
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                                                                                                                                                                                                         The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (8cFv) or a disulfide Fv (46Fv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer the medicament because and melanoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an cutte myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. It is the septements a human Fv molecule hypervariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GlyLys----GlyLeu----GluTrp11eGlyGluIleAsnHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                        Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guy R, Lipschitz O, Szanton E, Levanon A;
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13
13
0
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                       Claim 13; Page 193; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG91903 standard; protein; 97 AA
                                                                                                                                                                                                                                                                                                                                                                                             related peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ACAACCCGTCCCTCAAGAGT 81
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                                    (BIOT-) BIO-TECHNOLOGY GEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.20
65.62%
59.38%
70.14%
                                                            Hagai Y, Lazarovits J,
Plaksin D, Peretz T;
                                                                                                WPI; 2002-619166/66
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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infortant in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, inflammation, where the epitope is capable of being bound by an antibody, crit antigon-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune cell-tendrosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-rell-matrix, platelet-matrix, platelet- platelet adhesion or aggregation, for increasing continuity of tumour or leukaemia cells for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases canchase cancer, leukaemia, autoimmune diseases, inflammatory contineases such as myocardial infarction, retinopathic diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-cells interactions. This sequence represents a human antibody fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated epitope present on cancer cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mar-Haim H;
Levanon A;
                                                                                                                                                                                                                                                                                                                                                                  Novel isolated epitope present on cancer cells and important in physiclogical phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human germline heavy chain variable region gene segment #40
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Peretz T,
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Matches:
Conservative:
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Amit B, Kooperman L,
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                                                                                                                                                   (BIOT-) BIO-TECHNOLOGY GEN CORP.
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                                                         29-DEC-2000; 2000US-00751181.
29-DEC-2000; 2000US-0258948P.
31-DEC-2001; 2001WO-US049442
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                                                                                                                                                                                                            , Hagai Y,
Richter T,
                                                                                                                                                                                                                                                                                                         WPI; 2002-674776/72.
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                                                                                                                                                                                                               Lazarovits J,
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                                                                                                                                                                                                                                                   Szanthon E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                      comptising making chimerical antibodies contraining a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibody in comparison to germline canonical CDR structure types of human antibody so the basis for selection, for humanised antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species. The method is reliable for identifying suitable humanised antibodies that retain him antigen binding with low immunogenicity in humans, without the need for on-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for determining critically important amino acid residues in the framework sequences of humanised antibodies with suitable therapeutic properties. The antibody framework sequences between non-human and human antibodies. This sequence represents a human hashy chain variable region gene segment used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                        Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method of making a humanised antibody
Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preation of humanised antibodies
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                                                                                                                                             12-JUL-2001; 2001US-0305111P.
                        canonical CDR structure type.
                                                                                                                     12-JUL-2002; 2002US-00194975.
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                                                                       US2003039649-A1
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Best Local Similarit
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The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CD1 and CD2 regions of the VH or VL region of immunoglobulin gene and a fragment containing the CD3 region by PCR, respectively, producing VH and VL Inbraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents a protein of the invention.
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                                                                                        antibody library, CD1 region; CD2 region; VH region; VL region; immunoglobulin; CD3 region; TM1 scFv; human.
                                              Human protein relating to the invention SEQ ID NO:55
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Matches:
Conservative:
Mismatches:
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04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takayanagi
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                                                                                                                                                                                                               WO2003044198-A1.
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                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                              30-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu N,
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DB:
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Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
                                                                                                                                                                                                                                                                                                Computer optimization of physicochemical properties of comprises analyzing the interactions of amino acids at
                VEGF antibody heavy chain variable region VH_4-34.
                                                                                                                                                                                01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                       03-MAR-2003; 2003WO-US006598
                                                                                                                                                                                                                                                Lazar GA, Desjarlais JR,
                                                                                                                                                                                                                                                                         WPI; 2003-722066/68
                                                                                                        WO2003074679-A2.
                                                                                                                                                                                                                       (XENC-) XENCOR.
                                                                              Homo sapiens
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                                                                                                                                12-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (l) treating a patient suffering from or at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor; and (3) screening for substances (5) capable of inhibiting the cinteraction between lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (5) has cytostatic activity, and can be used in gene therapy, and as a glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence ceresents an Ig variable region sequence which is used in the cycentation of the present invention.
                                                                                                                                                                                                                                                                    Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma..
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Indels:
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                                                                                                                                                                                                                     Stevenson F;
                                                                                                                                                                                                                                             WPI; 2003-902720/82.
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                                                                                        WO2003074059-A2,
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                                                                Homo sapiens.
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antibodies variable

Marshall SA, Dahiyat B;

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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical property. The method is useful for optimizing solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody way be variable region sequence used to illustrate the invention.
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Indels:
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Matches:
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Example 6; Fig 16a; 135pp; English
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variable region; human.
                                                                                                                                              (XENC-) XENCOR
                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                  12-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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1D ADJ8

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                                                                                                                                                                                                                                                                                                    The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical properties of an antibody sepecially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
          Antibody; stability; solubility; antigen binding affinity; variable region; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; stability; solubility; antigen binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable region sequence used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
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                                                                                                                                                                                           Desjarlais JR, Marshall SA,
                                                                                                                                                                                                                                                                                  Example 16; Fig 40a; 135pp; English.
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                                                                                                                                   01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                              03-MAR-2003; 2003WO-US006598
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65.62%
59.38%
70.14%
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Best Local Similarity:
                                                                 WO2003074679-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97 AA;
                                                                                                                                                                     (XENC-) XENCOR
                                             Homo sapiens
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                                                                                       12-SEP-2003
                                                                                                                                                                                                                                                            positions.
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, especially or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 GlyLys----GlyLeu----GluTrpl1EGlyGluIleAsnHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nybrid antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2a; 135pp; English.
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                                                                                                                                                                               01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                     03-MAR-2003; 2003WO-US006598
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98.20
65.62%
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Best Local Similarity:
WO2003074679-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97 AA;
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Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M, 1gM; V gene diversity; directed constitutive hypermutation; target sequence diversification; terminal deoxynucleotidyl transferase; TdT; clonal expansion; selection; heavy chain variable region; VH;

Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N

18-SEP-2000 (first entry)

AAB01949;

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a trarget species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is alfferent than the first component to sequence of the second component to sequence so natibody fragment sequence database of antibody sequences or antibody fragment sequence attabase of antibody sequences or antibody fragment sequence attabase of antibody sequences from the database which demonstrates a high selecting a sequence from the database which demonstrates a high selected framework sequences from the database which demonstrates a high selected framework sequences to one or more complementarity determining antibody that the selected antibody; and (ix) operatively linking the selected framements are useful for therappeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibods that highly homologous and exhibit reduced immunogenicity while maintain the selective the CDRs. This produces antibods that high and a single maintain to receive the CDRs. This produces antibods and a single maintain to receive the CDRs. This produces antibods and a single maintain to receive the CDRs. This produces antibods and a single maintain the maintain and exhibit red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the VH gene locus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOLAN463-1B.SEQ (1-81) x ADJ80323 (1-97)
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                                                                                                            03-DEC-2002; 2002WO-US038450.
                                                                                                                                                         03-DEC-2001; 2001US-0336591P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.000883
                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC.
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65.62%
59.38%
70.14%
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Best Local Similarity:
Query Match:
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                     WO2003048321-A2
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The invention relates to a method of preparing a lymphoid cell line capable of directed constitutive hypermutation of a target capable of directed constitutive hypermutation of a target nucleic acid mutation sace screening a cell jopulation for ongoing target sequence diversification and selecting a cell in which the cate of target nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid mutation expressing a cell in which the capacing a gene product with a desired activity, comprising expressing a nucleic acid encoding the target gene operably linked to a sequence which directs hypermutation e.g., terminal deoxynucleotidyl expressing a mutated gene product with the desired activity. One cells with an improved activity of interest are selected. These steps may be iteratively repeated until a gene product with a desired of activity of sobtained. The cell lines prepared according to the method of the invention are used for directed constitutive hypermutation of a nucleic acid region in the preparation of a gene product, preferably an enzyme or an immunoglobulin (Ig) with a desired activity. In the exemplifications of the invention, IgM-secreting Ramos cells were selected for use as they undergo hypermutation during clonal expansion. This was determined on the basis of the amount of diversity in the heavy chain variable region (VH). Sequences AAB01949-B01954 which have lost the ability to bind anti-idotype antipodies (anti-ida Ab) relative to the will-type VH (AAB01948). Note: The present sequence is not shown in the specification, but is derived from the wild-type Ramos cell VH shown in figure 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphoid cell line preparation useful for producing gene products having desired activity, involves screening and selecting cells having ongoing target sequence diversification and higher mutation rates.
                                                                                                                                                                                                                                                                                                            /note= "Encoded by CAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sale JE, Neuberger MS, Cumbers SJ;
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page; 69pp; English.
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99GB-00001141.
99GB-00013435.
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N-PSDB; AAA52435.
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Misc-difference
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114

Alignment Scores: Pred. No.:

19	N	٣	80	0
Matches:	Conservative:	Mismatches:	Indels:	Gaps:
98.20	65.62%	59.38\$	70.14%	3
Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

NOLAN463-1B.SEQ (1-81) x AAB01949 (1-114)

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Search completed: August 4, 2005, 18:14:25 Job time: 93.5 secs

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140, App
22, Appl
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Appli
Appl
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Sequence 118, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Maceuda, Fuminiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: BEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
STREER: 225 Franklin Street
CITY: Boston
STREER: MA

COUNTRY: US

COUNTRY
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                                                                      US-09-372-425A-2
US-08-652-816A-13
US-08-918-148-79
US-08-918-091A-77
US-09-138-091A-77
US-09-126-219A-169
US-09-726-219A-169
US-09-726-219A-169
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-193
ATTORNEY, AGSNT THYORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELEPHONE: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-802-077-7
US-09-025-769B-39
US-09-0205-769B-65
US-09-490-070A-65
US-09-490-153-95
US-09-490-153-65
US-09-490-133-65
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US-08-851-362D-22
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US-09-802-096-7
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US-08-325-955-6
US-08-767-128-18
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US-09-273-453-7
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  TELEFAX: 617-9
TELEX: 200154
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  -WODEL-frame+ n2p.model -DEV=x1p
-WODEL-frame+ n2p.model -DEV=x1p
-WODEL-frame+ n2p.model -DEV=x1p
-Q=Cqn2_1/VSPTO spool_pYNOLANO8728463-1/runat_04082005_125807_24557/app_query.fasta_1.5
-DB=18sued Patents A. -OFMI-fastan -SUFFIX=rai -MINMATCH=0_1 -T.COPCIL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -THR MAX=100 -TRR MIN=0 -ALIGN=15
-MODE=LCGAL -OUTFWT=pto -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLANO8728463-1 @CGN 1 1 66 @runat_04082005_125807_24557 -NCPU=6 -ICPU=3
-DOW_MARP -LARGEQUERY -NES SCORES=0 -MAITT -DSPALOCK=100 -LONGLOG
-DOW_MARP -LARGEQUERY -LOS SCORES=0 -MAITREADS=1 -XCAPOP=10 -XCAPDEXT=0.1 -FGAPOP=6
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Sequence 2, Appli
Sequence 6, Appli
Sequence 25, Appl
Sequence 335, Appl
Sequence 335, Appl
Sequence 335, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 118, App
Sequence 4, Appli
                                                                                                                                                                            4, 2005, 18:05:28; Search time 23.25 Seconds (without alignments) 520.135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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1 CGGGCGAGTCAGGATATTAG.....ACAACCCGTCCTCAAGAGT
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                             protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-545-809A-118
US-08-793-450-4
US-09-203-768A-2
US-08-372-425A-6
US-09-025-769B-25
US-09-490-070A-25
US-09-490-153-25
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
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US-08-466-151-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match
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988.2
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998.2
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992.1
992.1
87.2
86.3
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                                                                                                                                                                                    Run on:
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Alignment Scores:
   Alignment Scores:
Pred. No.:
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US-08-793-450-8
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                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08793450
; Sequence 4, Application US/08793450
; Patent No. 6312690
; Patent Naration: Marcharitic Christial Applicant: Charlin, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS: 3
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; STREET: VA
; STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                             116
119
23
3
                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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98.20
65.62%
59.38%
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                   : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 123 amino acids
amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                               / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-545-809A-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-793-450-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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Pred. No.:
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                                     LENGTH:
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Sequence 2, Application US/09203768A
Patent No. 6787638
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: 1998-12-02
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08793450

Sequence 8, Application US/08793450

Patent No. 6312690

GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHMAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
119
3
8
0
123
119
2
3
8
8
                                Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Length:
Matches:
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Matches:
                                                                                                               NOLAN463-1B.SEQ (1-81) x US-08-793-450-4 (1-123)
                                                                                                                                                                                                             62 ACAACCCGTCCTCAAGAGT 81
                                                                                                                                                                                                                             62 ACAACCGTCCTCAAGAGT 81
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98.20
65.62%
59.38%
 7.89e-05
             98.20
65.62%
59.38%
70.14%
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US-09-203-768A-2
                       Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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JS-09-025-769B-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09372425A

Patent No. 6475749

GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
TITLE OF INVENTION: Improved Rh Antibody
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: LOS Angeles
STREET: CA Angeles
STREET: USA ANGELES
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTY: USA
ZIP: 90067
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ACAACCCGTCCCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAN: 703-413-2220
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.20
65.62%
59.38%
70.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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Best Local Similarity:
Query Match:
22202
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SOFTWARE: Petentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-PEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-MG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REJESTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1251 Avenue of the Americas
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09025769B
Fatent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: 1lag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION:
APPLICANT: Plueckthun, Andreas
TITLE OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Heavy chain without Tailpiece - AA
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORWATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMUNICATION INFORMATION:
TELEPRAX: (310) 788-5000
TELEPRAX: (310) 788-5000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acids
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.000592
93.20
65.62%
56.25%
66.57%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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SEQUENCE CHARACTERISTICS
                                                                                                                     JS-09-490-070A-25
                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy
                                                                                                                                                                                                                                                                                                                                                                GGCGAGTCAGGATATTAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-490-070A-25
i Sequence 25, Application US/09490070A
j Sequence 25, Application US/09490070A
j Fatent No. 6666248
j Fatent No. 6666248
j GENERAL INFORMATION: Peter
llag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
j ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
Milte & McAulliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D.C.
COUNTY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                             NOLAN463-1B.SEQ (1-81) x US-09-025-769B-25 (1-118)
                                                                                                                                                                                                                                                                                              Gaps:
            INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 118 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 25
 (212)596-9000
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50.00%
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Best Local Similarity:
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 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09490153
Fatent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Fack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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21
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19
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-FEB-1996
APPLICATION UNMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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                                     STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212):596-9000
TELEFAX: (212):596-9090
MATION FOR SEQ ID NO: 25:
LENGTH: 118 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 3 GGCGAGTCAGGATATTAGCAGC
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SEQUENCE CHARACTERISTICS
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50.00%
47.73%
65.79%
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COMPUTER READABLE FORM:
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STATE: New York
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Best Local Similarity:
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COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TAMPER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-490-324-25
: Sequence 25, Application US/09490324
; Patent No. 6828422
; Patent No. 6828422
; APPLICANT: Knappik, Achim
Pack, Peter
liag, vic Ge, Lining
Moroney, Simon
Plueckthun, Andreas
TITLE OP INVENTION: Protein/ (Poly) peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                     Gaps:
                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
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TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
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SEQUENCE CHARACTERISTICS:
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47.73%
65.79%
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                  26 GlyGlySer----lleSerSerTyrTyrTrpSerTrplleArgGlnProProGlyLysGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Horion, Taguku
APPLICANT: Horion, Taguku
APPLICANT: Matguda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOCLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: BOSTON
                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: DISKETE COMPUTER: DISKETE COMPUTER: Windows95

SOFTWARE: FASCESC for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                3 GGCGAGTCAGGATATTAGCAGC-------
                                                                                                                                                                                                                                                                                                                                  NOLAN463-1B.SEQ (1-81) x US-09-490-324-25 (1-118)
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-124-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 137, Application US/08545809A, Patent No. 6096878, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                        0.000517
92.10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
Query Match:
DB:
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US-08-545-809A-137
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 835, Application US/09471276
| Patent No. 6822072
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Gordano, J.Y.
| TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| Patent No. 6822072
| FILE REFERENCE: GENSET.025CP1 |
| CURRENT APPLICATION NUMBER: 09/09/471,276 |
| CURRENT FILING DATE: 1999-12-21 |
| EARLIER APPLICATION NUMBER: 09/057,719 |
| EARLIER PILING DATE: 1998-04-09 |
| EARLIER FILING DATE: 1998-04-09 |
| EARLIER FILING DATE: 1999-04-09 |
| SARLIER FILING DATE: 1998-04-09 |
| SOFTWARE: Patent.pm |
| SEQ ID NOS: 1622 |
| LENGING NOWERS |
| SARLIER FILING DATE: 1999-04-09 |
| SARLIER FILING DATE: 1990-04-09 |
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Matches:
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Mismatches:
Indels:
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Matches:
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US-08-466-151-5
; Sequence 5, Application US/08466151
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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sSer 84
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US-09-471-276-835
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Alignment Scores:
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DB:
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Matches:
Conservative:
Mismatches:
Indels:
GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STREET: USA
COUNTRY: USA
CITY: GA1080
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOLAN463-1B.SEQ (1-81) x US-08-466-151-5 (1-130)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
PRIOR APPLICATION NUMBER: 08/405617
PRIOR APPLICATION DATA: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA: 08/185899
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA: 07/879495
PRIOR APPLICATION NUMBER: 07/879495
PRIOR APPLICATION NUMBER: 07/879495
PRIOR APPLICATION NUMBER: 07/879495
PRIOR APPLICATION NUMBER: 07/8798
PRIOR APPLICATION NUMBER: 07/8798
PRIOR APPLICATION NUMBER: 07/8798
PRIOR APPLICATION NUMBER: 07/8798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
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Amino Acid
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61.64%
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Best Local Similarity:
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Sequence 5, Application US/09802077;
Sequence 5, Application US/09802077;
Batent No. 6699472;
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Penera, Leonard G.
TILE REPERENCE: P0718P2C2US
CURRENT PILLOR DATE: 2008
FILE REPERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 1995-01-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILLING DATE: 1994-01-26
PRIOR PILLING DATE: 1994-01-26
PRIOR PILLING DATE: 1994-01-26
PRIOR PILLING DATE: 1992-06-14
PRIOR PILLING DATE: 1991-06-14
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                               Alignment Scores:
Pred. No.:
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C3US
CURRENT PILING DATE: 2010-03-08
FRIOR PELLING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
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Matches:
Conservative:
Mismatches:
Indels:
US-08-466-163B-5

Sequence 5, Application US/08466163B

Patent No. 6329509

GENERAL INFORMATION:
APPLICANT: Jardieu, Peula M.
APPLICANT: Jardieu, Peula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1

CURRENT FILING DATE: 1995-06-06
PRIOR PILING DATE: 1995-06-06
PRIOR PILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR FILING DATE: 1994-01-26

PRIOR FILING DATE: 1991-08-14
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Best Local Similarity:
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Title: Perfect score: Sequence:

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10 192, Appl

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12, Appl

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11, Appl

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Fublication No. US20030059937A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/274,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
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US-09-880-748-1333
                                                     Result
No.
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-MODEL=frame+ n2p.model -DBV=xlp
-MODEL=frame+ n2p.model -DBV=xlp
-MODEL=frame+ n2p.model -DBV=xlp
-MODEL=frame+ n2p.model -DBV=xlp
-DB-Published Applications AA -OFMT=fastan -SUFFTX=rapb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT$=bits -START=1 -END=-1 -MATRIX=blosum62
-LTRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAX_EN=2000000000
-USRB=NOLMAN08728463-1 @CGN 1 1 260 @THNATA 1 -DSPBLOCE** 100 -LONGLOG
-USRB=NOLMAN08728463-1 @CGN 1 1 260 @THNATA 1 -DSPBLOCE** 100 -LONGLOG
-USRB=NOLMAN08728463-1 @CGN 1 1 260 @THRRADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-EGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                                                                      August 4, 2005, 18:20:25; Search time 80.25 Seconds (without alignments) 788.093 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                      CGGGCGAGTCAGGATATTAG.....ACAACCCGTCCCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Ggn2_6/ptodata/1/pubpaa/US07_PUBCCMB.ppp:"

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(ggn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:"

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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                         protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1752860 seqs, 390397842 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 200000000
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Sequence 1333, Application US/10293418
Publication No US20030223996A1
GENERAL INFORMATION:
APPELICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-010-16
PRIOR FILING DATE: 2000-010-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION PUBLICATION PUBLIC
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1333
LENGTH: 253
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; ORGANISM: Homo sapiens
US-10-293-418-1333
                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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---GGATAT 17
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                                                       18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA
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                                                                                                                                                                                   US-10-371-942-118

Sequence 118, Application US/10371942

Sequence 118, Application US/10371942

Publication No. US20030223994A1

GENERAL INFORMATION:
APPLICANT: Relear, Yoram

TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
FILE REFERENCE: 10280-034001

CURRENT PAPLICATION NUMBER: US 60/358,994

PRIOR APPLICATION NUMBER: US 60/358,994

PRIOR PILING DATE: 2002-02

PRIOR PILING DATE: 2002-02

NUMBER OF SEQ ID NOS: 121

SOFTWARE: FREESEQ for Windows Version 4.0
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22
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Matches:
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47.83$
71.36$
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; ORGANISM: Homo sapiens
US-10-371-942-118
 3 GGCGAGTCA-
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Best Local Similarity:
Query Match:
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Pred. No.:
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LENGTH: 125
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Sequence 40, Application US/10194975

Publication No. US20030039649A1

GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REPERENCE: 501231 01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 40
LENGTH: 97
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US-10-308-817-83
Sequence 83, Application US/10308817
Sequence 83, Application No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
                                                                                                                                                                                                                                                                                                                      59 yrAsnProSerLeuLysSer 65
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PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 80
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                 NOLAN463-1B.SEQ (1-81) x US-10-308-817-83 (1-97)
| FILE REFERENCE: 1087-37 | CURRENT APPLICATION NUMBER: US/10/308,817 | CURRENT PILLING DATE: 2002-12-03 | NUMBER OF SEQ ID NOS: 195 | SOFTWARE: Patentin version 3.1 | SOFTWARE: Patentin version 3.1 | LENGTH: 97 | TYPE: PRT | TYPE: PRT | CORGANISM: human US-10-308-817-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 87, Application US/10029988B; Publication No. US20040001839A1; GENERAL INFORMATION:
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US-10-032-037B-87
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Sequence 87, Application US/10029926B

Sequence 87, Application US/10029926B

Publication No. US20040073011A1

GENERAL INFORMATION:
APPLICANT: HAGAY, et al.
FILE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10799/50

CURRENT APPLICATION NUMBER: US/10/029,926B

CURRENT FILING DATE: 2001-12-31

PRIOR FILING DATE: 12/29/2000

NUMBER OF SEQ ID NOS: 203

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 97

TYPE: PRT
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Matches:
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Matches:
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             US-10-453-698-83

Sequence 83, Application US/10453698

Publication No. US20040038308A1

GENERAL INFORMATION:

APPLICANT: Rother, Russell

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 82 CIP (1087-37 CIP)

CURRENT APPLICATION NUMBER: US/10/453,698

NUMBER OF SEQ ID NOS: 196

SOFTWARE: Patentin version 3.2

SEQ ID NO 83

LENGTH: 97

TYPE: PT

ORGANISM: human

US-10-453-698-83
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Best Local Similarity:
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Pred. No.:
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US-10-032-423A-87

US-10-032-423A-87

Sequence 87, Application US/10032423A

Publication No. US20040002450A1

GENERAL INFORMATION:

TITLE OF INVENTION: Y1-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/032,423A

CURRENT FILING DATE: 12/29/2000

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR PILING DATE: 12/29/2000

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 87

LENGTH: -7
APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: X17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REPERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR APPLICATION NUMBER: 60/258,948
RIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 97
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: homo sapiens
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US-10-73-532-128

Sequence 128, Application US/10733532

Publication No. US20050026246A1

GENERAL INFORMATION:

APPLICANT: Sale, Julian E.

APPLICANT: Neuberger, Michael S.

APPLICANT: Cumbers, Sarah J.

TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2002B

CURRENT APPLICATION NUMBER: US/10/733,532

CURRENT FILING DATE: 2003-12-11

PRIOR APPLICATION NUMBER: PCT/GB02/0268B

PRIOR FILING DATE: 2002-06-11

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-11

NUMBER OF SEQ ID NOS: 130

SEQ ID NO 128

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Mismatches:
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US-10-379-392-47

Sequence 47, Application US/10379392

Publication No. US20040110226A1

GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Debjarlais, John Rudolf
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILLE REPRENCE: A-71386-3 463077-236

CURRENT APPLICATION NUMBER: US/10/379,392

CURRENT APPLICATION NUMBER: US 60/360,843

PRIOR PILING DATE: 2002-03-01

PRIOR PILING DATE: 2002-03-01

PRIOR FILING DATE: 2002-03-01

PRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: Patentin version 3.2

LENGTH: 97
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
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RESULT 15

US-09-864-761-44315

US-09-864-761-44315

is Sequence 44315. Application US/09864761

j Patent No. US20020048763A1

j GENERAL INFORMATION:

j APPLICANT: Penn, Sharton G.

j APPLICANT: Rank, David R.

j APPLICANT: Hanzel, David R.

j APPLICANT: Chen, Wensheng

j TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBNESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                US-10-898-408-12

| Sequence 12, Application US/10898408
| Publication No. US20050058642A1
| GENERAL INFORMATION:
| APPLICANT: GALIBERT, Laurent J.
| APPLICANT: GALIBERT, Laurent J.
| APPLICANT: YAN, Wei
| TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
| FILE REFERENCE: 3467-A
| CURRENT PILING DATE: 2004-07-23
| PRIOR APPLICATION NUMBER: 60/490,027
| PRIOR FILING DATE: 2003-07-25
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 12
| LENGTH: 115
                                                                                                                                                                                           42 GlyLys----GlyLeu----GluTrplleGlyGluIleAsnHisSerGlySerThrAsnT 59
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Mismatches:
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Cincesion: B49028
Ritimers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur.
Bur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob A;Reference number: A49028, MUID:92008140; PMID:1915549
A;Reference number: B49028
A;Recession: B49028
A;Residues: 1-143 - TIM>
A;Residues: 1-143 - TIM>
A;Residues: 1-131 - T
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Ig gamma chain V r
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B49028
C;Species: Homo eapiens (man)
C;Species: Homo eapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
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                                                          Alignment Scores:
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1 CGGCCGAGTCCAGGATATTAG.....ACAACCCGTCCCTCAAGAGT
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(c) 1993 - 2005 Compugen Ltd
                                                                                             protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                  of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                283416 segs, 96216763 residues
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JL0047
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A49045
PS3341
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S78055
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, Delext
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Maximum Match 100%
Listing first 45 80
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length: 200000000
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Database

Total number

Searched:

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Result õ

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C;Accession: 837454
R;McIntobab, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from p. A;Reference number: 837453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                       42 GlyLys----GlyLeu----GluTrpl1eGlyGluIleAsnHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S;806
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                   A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377 C;Superfamily: immunoglobulin V reggion; immunoglobulin homology C;Koyeords: heterotetramer; immunoglobulin F;15-97/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gross references: EMBL:X75022; NID:9404311; PIDN:CAA52930.1; PID:9758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
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Matches:
Conservative:
Mismatches:
Indels:
                 Conservative:
Mismatches:
Indels:
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65.62%
59.38%
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-106 <MCI>
                 Percent Similarity:
Best Local Similarity:
Query Match:
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A;Molecule type: DNA
A;Residues: 1-97 <WEN>
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A; Reference number: 812420
A; Reference number: 812420
A; Retense translation not shown
A; Molecule type: DNA
A; Residues: 1-97 < csANA
A; Crose-references: EMBL: X56364
A; Experimental source: V(H) 4.2
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology < IMM>
                                         S26805
Ig heavy chain V region - human
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens
C;5pecies: D.M.
A;7tcle: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;7tcle: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;7cces-references: RBBL: 214241; NID: g377714; PIDN: CAA78610.1; PID: g1335376
C;5uperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C; Secesian S26898; S12420
C; Accession: S26898; S12420
C; Accession: S26898; S12420
A; Tomlinson, I.M.; Walter, G; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Tomlinson, I.M.; Walter, G; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Title: The repertoire of human germline V(H) sequences reveals about fifty gro
A; Reference number: S26885; MUD:93021117; PMID:1404388
A; Accession: S26898
A; Molecule type: DNA
A; Residues: 1-97 <TOMA
A; Residues: 1-97 <TOMA
A; Residues: Eferences: EMBL:21363; NID:932944; PIDN:CAA78233.1; PID:932945
A; Sanz, I; Kelly, P:; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-13748, 1989
EMBO J. 8, 3741-13748, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
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37.74%
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DB:
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Alignment Scores:  Pred. No.:  Score:  Score:	PBSULT 8  RESULT 8  S78052  Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man) C;Species: How-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78052; S23717 R;Harindranath, N. Submitted to the EMBL Data Library, August 1990 A;Reference number: S78051 A;Accession: S78052 A;Molecule type: mRNA A;References: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118 R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991 A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.	A; Reference number: S23716; MUID:92031262; FMID:1718404 A; Accession: S23717 A; Molecule type: mRNA A; Residues: 15-111 < HAM> A; Cross-reference: EMBL:X54441 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin V region; fattus predicted <sig>F;1-14/Domain: signal sequence (fragment) #status predicted <nat>F;29-111/Domain: immunoglobulin homology <inm></inm></nat></sig>	Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Best Local Similarity:  Query Match:  2 Gaps:  O.000301  Length:  Matches:  Conservative:  Mismatches:  Indels:  Gaps:  O.000301  Length:  Matches:  19  Conservative:  Anilarity:  70.14  Indels:  O.000301  Matches:  O.	NOLAN463-1B.SEQ (1-81) x S78052 (1-140)   OY	RESULT 9 A49045 19 heavy chain V region (anti-B cell autoantibody) - human (fragment) C;Species: Homo sapiens (man) C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999 C;Accession: A49045 R;Accession: A49045 R;Accession: A49045 R;C; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma Bur. J. Immunol. 22, 1781-1788, 1992 A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
Score:   98.20   Matches:   19   Percent Similarity:   65.62%   Conservative:   2   Best Local Similarity:   59.38%   Mismatches:   3   Mismatches:   3   Tol.14%   Indels:   8   Tol.14%   Tol.14	RESULT 6 JL0047 JL0047 JL0047 JL0047 JL0047 G. Jacus Homo sapiens (man) C. Species: Homo sapiens (man) C. Species: Homo sapiens (man) C. Jace: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996 C. Accession: JL0047 R. Jectster, A.; Lavenir, I.; Rabbitts, T.H. J. Exp. Med. 167, 2011-2016, 1988 A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new A; Reference number: JL0047; MUID:88258392; PMID:3133445 A; Reference number: JL0047; MUID:88258392; PMID:3133445 A; Residues: 1-122 - RAE> A; Residues: 1-122 - RAE> A; Residues: T-cell line RPMI 8402 A; Note: the authors translated the reading frame which extends to the stop codon; the A; Note: this sequence belongs to the VH II subgroup C; Superfamily: immunoglobulin vegion; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology  F;23-105/Domain: immunoglobulin homology	Alignment Scores: 0.000299 Length: 122 Pred. No.: 98.20 Matches: 19 Score: Percent Similarity: 65.62% Conservative: 2 Best Local Similarity: 59.38% Mismatches: 3 Query Match: 2 Guery Match: 2 Guery Match: 2 Guery Match: 2 Guery Match: 170.14% Indels: 8 DB: 2 Gaps: 0	Oy         2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATC	RESULT 7 S47010 Igh heavy chain V4.21-UniqueD-J5 region - human C; Species: Homo sapiens (man) C; Accession: 847010 C; Accession: 847010 R; Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E. submitted to the EMBL Data Library, July 1994 A; Appertiption: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin	A;Accession: S47010 A;Accession: S47010 A;Accession: S47010 A;Status: preliminary A;Accession: S47010 A;Cross-creferences: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255 A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology cIMM> F;15-97/bomain: immunoglobulin homology cIMM>

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C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
Limmunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals apply A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin B;9-38/Region: framework 1 F;9-38/Region: complementarity-determining 1 F;44-57/Region: framework E;88-74/Region: framework E;58-74/Region: complementarity-determining 2 F;75-106/Region: framework 3
  A; Reference number: PS0341; MUID: 92171937; PMID: 1540170
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Matches:
Conservative:
Mismatches:
Indels:
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89.47$
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94.20
62.50%
56.25%
67.29%
                      A, Accession: PS0341
A, Molecule type: mRNA
A, Residues: 1-133 <RAT>
                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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A; Residues: 1-97 <SAN>
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1g heavy chain V-D-J region (RAMOS) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997

C;Accession: PS0341

R;Ratech. H.

Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992

A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B2346
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A;Lieoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A;Tile: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23346
A;Accession: B23346
A;Accession: B23346
A;Accession: B23346
A;Residues: 1-231 <LEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DAB
A;Residues: 1-140 cGRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Cross-reference extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Indels:
Gaps:
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Best Local Similarity:
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Pred. No.:
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DB:
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81 73

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C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                           94
18
8
8
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Matches:
Conservative:
Mismatches:
Indels:
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24 61

1 20 1

Conservative: Mismatches: Indels: Gaps:

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C;Accession: $14474
$Yan Bs, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
submitted to the EMBL Data Library, November 1990
A;Reference number: $14474
                                                                                                                                                                                                                                    42 GlyLys----GlyLeu----GluTrplleGlyGluIlelleHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C'Species: Homo sapiens (man)
C'Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 GlyGlySer----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 4, 2005, 18:21:23
Job time : 18.25 secs
                                                                                                             NOLAN463-1B.SEQ (1-81) x S78055 (1-145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOLAN463-1B.SEQ (1-81) x S14474 (1-97)
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                                                                                                                                                     GGCGAGTCAGGATATTAGCAGC
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    48.89%
46.67%
65.71%
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62.50$
56.25$
63.71$
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uLysSer 83
  Percent Similarity:
Best Local Similarity:
Query Match:
D8:
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A, Molecule type: DNA
A, Residues: 1-97 <ESJ>
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Best Local Similarity:
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Pred. No.:
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A; Residues: 1-145 < HAR>
A; Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
A; Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
B; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-98 «TOM»
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
ENSOnz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
ENBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; WUID:90059975; PMID:2511001
A;Accession: S12419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 sGlyLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLe 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: Howo-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78055; S23720 R;Harindranath, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyGlySer----IleSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy
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A; Residues: 18-115 < HAW>
A; Cross-references: EMBL:X54445
A; Note: the authors translated the codon GCA for residue 67 as Arg
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>F;1-15/Product: Ig heavy chain (fragment) #status predicted <MAT>F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                   C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
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21
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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A;Reference number: S78051
A;Accession: S78055
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92.00
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uLysSer 66
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Best Local Similarity:
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Length: Matches: Conservative: Mismatches: Indels:

Gaps:

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TISSUE-Hodgkin lymphoma;
Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R., Hansmann M.L., Brauninger A.;
Hansmann M.L., Brauninger A.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564425; CAD92032.1; -.
HSSSP; P18532; IKCV.
InterPro; IPR003109; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
          066gmx1
0611713
072373
072373
072373
0926x8
066tjd4
066tjd4
066tjd6
066tjd4
066tjd7
096tjd7
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 Q9u173
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119
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                             Q7Z379
HV47 MOUSE
Q99CA9
                                                                                                                                                                                                                                                       Q80632
Q6LBQ5
HV46_MOUSE
Q7ZB<u>8</u>2
                                                                               06TJQ4
090QV6
096KX8
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Q6QJ62
Q99CH3
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09IUP1
09IUR6
07ZN97
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Q9J783
Q9IUT6
Q9IQS9
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090KY2
090KY3
0698Z8
Q9UL73
Q6GMX1
                      Q6NYH3
095973
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65.62%
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Homo sapiens (Human)
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Best Local Similarity:
                                                                                                                  NCBI_TaxID=9606;
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116 A
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
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mus musculu
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                                                                             4, 2005, 17:55:57; Search time 83.75 Seconds (without alignments) 990.529 Million cell updates/sec
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                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                       CGGGCGAGTCAGGATATTAG.....ACAACCCGTCCCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGGMX5
O9bul0
O96aa6
O9bqb8
O6p4i8
P06331
O6gmx7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96ey0
Q99m22
P18532
Q6gmx6
Q65zi1
P18531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O8wux4
                                                                                                                                                                                                                                                                               3224756
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                        protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                072316
08WUX4
06GWUX5
06BWUX6
09BU10
09BQBB
06P418
06P418
06CWX7
06GWX7
096EX0
099M22
HV61_MOUSE
06GWX6
06GWX7
HV61_MOUSE
                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                            ----
                                                                                                                                                                                         Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: uniprot sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length DB
                                                                                                                               NOLAN463-1B.SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
620
479
116
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                                                                                  August
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50.9
                                                                                                                              Title:
Perfect score:
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998.2
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Maximum DB
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                                                                                  Run on:
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No.
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N

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TISSUE=Lymph;
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                                                                                   85
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                                                                                                                                      RESULT 3
                                                                                                                                                                 Q6GMX5
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 34964; AAH19235.2;
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
Ffam; PR07654; C1-set; 4.
SMART; SM00409; 1G9; 2.
SMART; SM00406; 1G9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
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                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                         PRT;
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                                                                                   81
                                                                                                           Ol-WAR-2004 (TERBLIFE). 20, C)
Ol-WAR-2004 (TERBLIFE). 26, La
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metall
                                                                                   ACAACCCGTCCCTCAAGAGT
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65.62%
59.38%
70.14%
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                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                   62
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QUANTA

QUAN
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61

68 GlyLyg----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85 

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, BCO73767; AAH73767-1; -.
R InterPro; IPR001599; IG-
R InterPro; IPR001599; Ig-
R InterPro; IPR003599; Ig-
R InterPro; IPR003596; Ig-
R InterPro; IPR003569; Ig-
R InterPro; IPR003569; Ig-
R InterPro; IPR003569; Ig-
R Ffam; PF07654; C1-set; 4.
R SWART; SW00409; IG-1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597
22
33
8
                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypoteatical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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81
                62 ACAACCCGTCCTCAAGAGT
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98.20
65.62%
59.38%
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                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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RESULT 5
                                                                       096AA6
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                                                                                                                                                                                                                                               MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MALGAUS R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., MaxS.I., Wang J., Halber F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyviki S., Carninoi P., Parage C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzry K.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Marywinski M.I., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
M. Krzywinski M.I., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO/bba, --
SMO0406; IGV; 1.
'E; PS50835; IG LIKE; 5.
'E; PS00290; IG MHC; UNKNOWN 3.
'E; PS00290; IG MHC; UNKNOWN 3.
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22
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0
                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
                                                                                                        597 AA.
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                                   8
                                                        84
                                               62 ACAACCCGTCCCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PP07654; C1-8et; 4
                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
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65.62%
59.38%
70.14%
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                                                                                                       PRELIMINARY;
                                                                                                                                                                 IGHM protein.
Homo sapiens (Human)
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Query Match:
DB:
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             61
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                                                                                                        Q9BU10
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TISSUB-Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutferfield Y.S.,

B Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.2; --
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WN 3.
F62FAB3ADE7ECBFE CRC64;
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                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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PROSITE; PS00290; IG MHC; UNKNOWN
SEQUENCE 625 AA; 68610 MW; P62
ACAACCGTCCCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; 19.
InterPro; IPR003599; 19.-1ike.
InterPro; IPR003597; 19_c1.
InterPro; IPR003696; 19_whC.
InterPro; IPR003696; 19_w.
Pfam; PF07654; C1-8et; 4.
SMART; SM00407; 1G21; 4.
SMART; SM00407; 1G21; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.000985
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65.62%
59.38%
70.14%
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                       IGHM protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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     62
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                                                                                                                                                                                              Q96AA6;
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NOLAN463-1B.SEQ (1-81) x Q96AA6 (1-625)

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Name=IGHD;
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                                                                                                                  Q6P4I8
                                                                                 RESULT 7
                                                                                                 Q6P4I8
ID Q6
                                                                                                                                   셤
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**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
**Altannar R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
**Altschul S.F., Zeeberg B., Buerchw K.H., Schaefer C.F., Bhat N.K.,
**Altschul S.F., Zeeberg B., Buerchw K.H., Schaefer C.F., Bhat N.K.,
**A Altschul S.F., Zeeberg B., Buerchw K.H., Schaefer C.F., Bhat N.K.,
**A Altschul S.F., Zeeberg B.B., Bonaldo M.F., Carnhon G.M., Hong L.,
**A Stapleton M., Soares M.B., Bonaldo M.F., Carnhon P.L., Scheetz T.E.,
**Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhon P.D., Prange C.,
**Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
**Bosak S.A., McKeman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
**Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
**Parker J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
**Rrzyminski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
**A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
**A Tonchman M.A.,
**Jones S.J., Marra M.A.;
**T "Generation and initial analysis of more than 15,000 full-length human and mouse on the state of the state of
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Strausberg R.;
L Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; GC06180; AAH06180.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003106; Ig-MC.
R InterPro; IPR003106; Ig-MC.
R InterPro; IPR003106; Ig-W.
R InterPro; IPR003106; Ig-W.
R EMBL; SNART; SNA0406; IG-Y.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG-MC; UNKNOWN 3.
SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
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118
2
4
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                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                  597 AA.
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                                                 62 ACAACCCGTCCCTCAAGAGT 81
                                                                  01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00622
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62.50%
56.25%
65.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                  IGHM protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Pred. No.:
                 68
                                                                                 85
                                                                                                                                                  Q9BQB8
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RX TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeborg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschako L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Eapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RY Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Gringuez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

RA Jones S.J., Marra M.A.;

RGeneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW 2.
FBE97C949D720F1E CRC64;
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                            576 AA
                                                                                                                                                                                                                                       Created)
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SW00406; IGV; 1.

PROSITE; PSS0835; IG_LIKE; 4.

PROSITE; PS00290; IG MHC; UNKNOWN

SEQUENCE 576 AA; 63363 MW; FBB
81
                           InterPro; IPR003599; IG.
InterPro; IPR003109; Ig-like.
InterPro; IPR003509; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF007654; C1-set; Z.
Pfam; PF0047; ig; 1.
SMART; SM004009; IG; 1.
SMART; SM004007; IGc1; 3.
62 ACAACCCGTCCCTCAAGAGT
                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC063384; AAH63384.1;
HSSP; P01820; 1A7N.
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48.89%
46.67%
65.71%
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                             IGHD protein.
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NOLAN463-1B.SEQ (1-81) x Q6P4I8 (1-576)

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0.135
82.10
47.73$
43.18$
58.64$
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TISSUE-Primary B-Cells,
                                                   Hypothetical protein.
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477 AA; 5
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                                                                                                                           NCBI_TaxID=9606;
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WE SEQUENCE FROM N.A.

WADLINE-85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;

WA KUGO A., Ishihara T., Nishimura Y., Watanabe T.;

Wido A., Ishihara T., Nishimura Y., Watanabe T.;

T. A Cloned human immunoglobulin heavy chain gene with a novel direct-
tr repeat sequence in 5' flanking region.";

T. repeat sequence in 5' flanking region.";

R. A01010; G1HUH2.

R. RSP; PO1825; FRAB.

R. RSSP; PO1825; FRAB.

R. GO; GO:000555; F:ammune response; NAS.

R. GO; GO:0006555; P:ammune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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118
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Matches:
Conservative:
Mismatches:
Indels:
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1IG heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                       146 AA
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                                                                                                                                                                                                                                                       PRT;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
GGCGAGTCAGGATATTAGCAGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ACAACCCGTCCCTCAAGAGT
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59.38%
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115
146
                                                                                                                                          75 CAAGAGT 81
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90 uLysSer 92
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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P06331;
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DISULFID
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SEQUENCE
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Q6GMX7;
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HV2I HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X TISSUBE-PILMARY B-Cells;

X Klausberg R.L., Feligoid E.A., Grouse L.H., Derge J.G.,

X Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninori P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia M., Gay L.J., Hulyk S.W.,

Yullalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G.,

Rodriguez A.C., Grimwood J., Schuuz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 yLeuGluTrpIleGlyTyrIleSerHisSerGlySerThrThrTyrAsnProSerLeuLy
                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberger R:
Submitted (JUN 2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073765; AA473765.1; -.
RINGERPO; IPR003599; IG.
InterPro; IPR003599; IG.
RINGERPO; IPR003599; IG.
RINGERPO; IPR003596; IG.
RINGERPO; IPR003596; IG.
R Pfam; PPC0047; IG.
R Pfam; PPC0047; IG.
R SMART; SM00409; IG; 4.
SMART; SM00406; IG; 1.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS50835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4477
22
44
119
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GlyGlySer----ileSerSerTyrTrpSerTrpIleArgGlnProProGlyLysGl
                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MRR-2004 (TrEMBLrel. 25, Last annotation update)
Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                             Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7D1E2302410E4F8C CRC64;
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2 2 4 199
6 119
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GGCGAGTCAGGATATTAGCAGC-----
                                                                          139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
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                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOLAN463-1B.SEQ (1-81) x Q86SX2 (1-139)
                                                                                                                                                                                       Homo sapiens (human) (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 139 AA; 15573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; IGv; 1.-
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.289
79.10
47.73%
43.18%
56.50%
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                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                         TISSUE=B cells;
Li W.B., Gruber C.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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sSer 84
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=B cells;
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83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                            Q86SX2;
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                                                                          Q86SX2
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                                                         Q86SX2
                                                                            SO DRAPA REPORTED DE LA PROPERCION DE LA
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Rischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., J. Jones S.J., Marra M.A.; and mouse chan alysis of more than 15,000 full-length human and mouse chan and smalls and seminars and seminar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buks musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; 1PR00110; 1g-like.
InterPro; 1PR003599; 1g.
InterPro; 1PR003599; 1g-like.
InterPro; 1PR003599; 1g-like.
InterPro; 1PR003596; 1g-d.
InterPro; 1PR003596; 1g-w.
Pfam; PR07654; Cl-set; 4.
SMART; SM00409; 1G, 2.
SMART; SM00400; 1G-like.
SMART; SM00406; 1G-y.
PROSITE; PS00393; 1G-Like; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; BC011857; AAH11857.2; -.
PIR; S15590; S15590.
HSSP; P01820; 1G7J.
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119
119
119
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA
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45.45$
43.18$
55.07$
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musculus (Mouse).
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STRAND
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SEQÜENCE
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ID QGGMX6
AC QGGMX6;
DT 05-JUL-2
DT 05-JUL-2
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DB:
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                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,

MI Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mothins K.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Man S.E., Loquellan K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carnincin P., Prange C.,

Man S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,

T. Generation and initial analysis of more than 15,000 full-length human

mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGCTGGTTAGCCGAAATC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: |||||| :::|||
31 LysProSerGinSerbeuSerbeuThrCysSerValThrGlyTyrSerIleThrSerGly
                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 AATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 AsnTyrAspGlySerAsnAsnTyrAsnProSerLeuLysAsn 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 479 Aa; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479
15
5
7
27
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV61 MOUSE STANDARD; PRT; 116 AA. P1853; 01-NOV-1990 (Rel. 16, Created) 01-NOV-2090 (Rel. 16, Last sequence update) 01-NOV-2004 (Rel. 45, Last annotation update) 19 heavy chain V region 1B43 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                 STRAIN=mix FVB/N; TISSUE=Mammary tumor;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR007110; Ig-like.
Interpro: IPR003597; Ig_ cl.
Interpro: IPR003595; Ig_ mHc.
Interpro: IPR003596; Ig_ MHc.
Interpro: IPR003596; Ig_ W.
Pfam; PP07654; Cl-set; Z.
SWART; SW0406; IGV.
PROSITE; PS06035; IG_ LIKE; 4.
PROSITE; PS060290; IG_ MHC; UNKNOWN_2.
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37.04%
27.78%
54.50%
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Pred. No.:
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HV61_MOUSE
ID HV61_MC
AC P18532;
DT 01-NOV-
DT 25-CCT-
DE 1g heav
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----AGCTGGTTAGC 32
                                                                                                                    Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                      primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region 1B43. Framework-1.
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16
3
13
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PDB; 1KCS; X-ray; H=19-116.
PDB; 1KCS; X-ray; H=19-116.
InterPro; IPR007110; Ig-like.
InterPro; IPR0071596; Ig_v.
SMART; SMO0406; IGv; 1.
PROSTTE; PS50835; IG_LKE; 1.
3D-structure; Immunoglobulin V region; Signal.
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(TrEMBLrel. 27, Last sequence update)
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Matches:
Conservative:
Mismatches:
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By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOLAN463-1B.SEQ (1-81) x HV61_MOUSE (1-116)
                                                                                                  MEDLINE=89279149; PubMed=2499654;
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75.70
56.76%
43.24%
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                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                     NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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05-JUL-2004
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Search completed: August 4, 2005, 18:20:08 Job time : 85.75 secs
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                                                                                                                                                                                        CTISSUBE-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSPER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Datchenko, L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Brahleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hae S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketreman M., Madan A.M., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

C. Animwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

C. Mones S.J., Marra M.J.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO3766; AdH3766.1;
InterPro; IPR003110; Ig-like.
InterPro; IPR003599; Ig c1.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig V.
Pfam; PF07654; C1-set; 3.
Pfam; PF07654; C1-set; 3.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 2.
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116
6
8
0
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
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Indels:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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75.20
56.25%
50.00%
53.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
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                       Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                         NCBI_TaxID=9606;
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Q65211;
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ID Q6
DDT REPARED BY SECOND BY S
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178 SerGlyTyr-TrpAsnTrpIleArgLysPheProGlyAsnLysLeuAspTyrMetGlyTy 197
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                                                                                                                                                                                                                                        TISSUE-Hybridoms;

MEDLINE-96211469; PubMed-8648670;

MEDLINE-96211469; PubMed-8648670;

Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;

Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;

Targeting human immunodeficiency virus type 1 reverse transcriptase by intracellular expression of single-chain variable fragments to inhibit early stages of the viral life cycle.";

J. Virol. 70:3392-4400(1996).

EMBL; U48716; AAB64342.1; -.

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

InterPro; IPR003599; Ig..

InterPro; IPR003599; Ig..

InterPro; IPR003598; Ig..

InterPro; IPR003596; Ig..
                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7DF20138E53865E4 CRC64;
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16
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112
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Matches:
Conservative:
Mismatches:
Indels:
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SWART; SWO0409; IG; 2.
SWART; SWO0408; IGC2; 2.
SWART; SWO0406; IGV; 2.
PROSITE; PS50835; IG LIKE; 2.
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72.80
55.56%
44.44%
52.00%
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SEQUENCE 262 AA;
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                                                                                                                                                                    NCBI_TaxID=10090;
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DB:
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Anti-huma
Human mAb
Human ant
                                       Human pho
Human pho
Human pho
Human leu
Hcw El an
Human ant
Human Fv
Human Fv
Human ant
Antibody
Antibody
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Anti-huma
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Anti-huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-murine CTLA-4 sFv; M24 sFv; single chain antibody; murine CTLA4; membrane-associated protein; chimeric construct; extracellular domain; human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7; recipient CD28; T-cell proliferation; xenograft-specific immunosuppression.
 Adk18895
Add18826
Add28826
Adp47098
Adp47098
Adp47099
Adp76561
Abd76231
Abd78233
Abd78233
Abd78233
Abd78233
Adk18898
Adk18899
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/note= "Corresponds to atc codon"
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                            ADP22194
ADP4708B
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ADP67621
ABG76561
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ADR46847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-murine CTLA-4 M24 8Fv
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 Dorling A;
 Key
Misc-difference
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AAY15128;
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-MODEL=frame+_n2p.model -DEV=xlp
-G/Gqn2_1/USFPO spool_p/NoLANB0728463-2/runat_04082005_123943_22574/app_query.fasta_1.5
-G/Gqn2_1/USFPO spool_p/NoLANB0728463-2/runat_04082005_123943_22574/app_query.fasta_1.5
-DB=A_GGReseq_OFMT=fastan -SUFPIX=rag -MINMATCH=0.1 -LOOPCL=0_-LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=pct -NONPM=ext - HarbasInz=500 -MINNENN=0 -ARIGN=15 -MODE=LOCAL
-USRB=NOLAN08728463-2 @CGN 1_1 308 @cunat 04082005_123943_22574 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELDEXT=0.1
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Aab70844 SNV-env l
Adr48005 Human mon
Adr46821 Human ant
Adr46819 Human pBl
Adr46817 Human bet
Adp47114 Human bet
Adp47114 Human pho
Adk18605 Anti-huma
Adk18791 Anti-huma
                                                                ; Search time 90 Seconds (without alignments) 721.953 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                            1 ATCATCTATCCTGGTGACTC.....GTATTAGCAGCTGGTTAGCC
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                protein search, using frame_plus_n2p model
                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                            2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
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ADR46829
ADR46819
ADR46827
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, Ygapext
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length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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This invention describes a novel cell-targeting vector (A) containing a CC DNA sequence (I) encoding a single-chain variable antibody fragment (SDNA sequence (I) encoding a single-chain variable antibody fragment (SDNA). The products of the invention have antiviral, cytostatic and immunostimulant activity and can be used in gene therapy, immunization and diagnosis particularly of T cell-associated diseases, specifically acquired immune deficiency syndrome (AIDS), severe combined immune to deficiency (SID) or T cell lymphoma. (A) target T cells, independently of the CD4 receptor, with high selectivity, 4-5 fold selectivity over three CC designated 7A5 encodes a 329 amino acid single-chain variable antibody fragment, fully defined in the specification. It was used to transform CD7 (canine osteosarcoma cells susceptible to spleen necrosis virus (SNV) cells, CB166 (human T lymphocyte) cells, and HeLa (human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to determine transformation. The viral liter (infectious units/ml) was over 1 million for D17, 1 million for CB166 but less than 100 for HeLa, showing the high selectivity for human T cells. This sequence represents the SNV-env leader/human 6C3-scPv fusion construct used in the invention. CU (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                             Cell-targeting vector selective for T lymphocytes, useful in gene therapy of e.g. acquired immune deficiency syndrome, encodes a single-chain variable antibody fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 AspThrAlaMetTyrTyrCysAlaArgValSerGlyTyrCysSerSerThrSerCysTyr 156
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Matches:
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Mismatches:
Indels:
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/label= SNV-env_leader
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                             Location/Qualifiers
                                                                             46. .302
/label= 6C3-scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 5; 18pp; German.
                                                                                                                                                                                                                                                                                                 Engelstaedter M;
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19.38*
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70.888
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Best Local Similarity:
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Chimeric
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                                                                                                                          The present sequence is the anti-murine CTLA-4 sFV (M24 sFV). This is a membrane-associated protein which binds to CTLA-4. Chimeric constructs comprising DNA sequences encoding the extracellular domain of murine CTLA4 and human CDB were used for the study of anti-CTLA4-sFV protein. The anti-hCTLA4 sFV functions as a ligand binding to CTLA-4 on activated T-cells and antagonises the co-stimulatory signal provided by the interaction between donor B7 and recipient CD28. Cells expressing the anti-hCTLA4 sFV failed to stimulate T-cell proliferation. This is used in xenograft-specific immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AspThrAlaValTyrTyrCysAlaArgPheSerLeuGlyGlyPheAspTyrTrpGlyGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GlyThrLeuValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGly 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 SerAlaLeuAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerValGlyAsp 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting T-cell mediated rejection of xenotransplanted organs
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11
189
                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                              Claim 9; Fig 11; 43pp; English.
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23.08%
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               2000-038815/03.
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                               N-PSDB; AAZ29000
                                                                                                                                                                                                                                                                                                 Sequence 240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human monoclonal antibodies or their antigen binding portions that specifically bind to dendritic cells and has one or more of the following characteristics: (a) a binding affinity constent to a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen binding portion may also have any of the following characteristics: (a) mediates cytolysis of dendritic cells in the presence of human effector cells; or (b) inhibits growth of dendritic cells. The antibodies or its antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, antiinflammatory, antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,
                                   157 AspTyrTyrTyrTyrMetAspValTrpGlyArgGlyThrLeuValThrValSerArg 176
                                                                                    177 GlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAsplleValMetThr 196
                                                                                                                                    .97 GlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrMetThrCysArgAla 216
                                                                                                                                                                                                                                                                                                                                                     cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human monoclonal antibodies specific for dendritic cells, useful for inhibiting growth or inducing cytolysis of a dendritic cell and treating or preventing a dendritic cell mediated disease, e.g., autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                   Human; monoclonal antibody; B11; antigen binding portion; dendritic
                                                                                                                                                                                                                                                                                                                                                                mannose receptor; growth; cytolysis; pathogen; virus; bacterium; autoimmune disease; inflammatory disorder; rheumatoid arthritis; autilipe sclerosis; diabetes mellitus; immunomodulatory; antiinflammatory; antiinflammatic; neuroprotective; antiabetic; antianemic; endocrine; dermatological; antithyroid; uropathic; ophthalmological; muscular.
                                                                                                                                                                                                                                                                                                                         Human monoclonal antibody B11 variable heavy chain protein.
                                                                                                                                                                                84
                                                                                                                                                                 58 AGTCAGGGTATTAGCAGCTGGTTAGCC
                                                                                                                                                                                                                                             AAM48005 standard; protein; 116 AA
                                                                                                             52 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 13; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001; 2001WO-US015114.
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                                                                                                                                                                                                                                                                                                (first entry)
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N-PSDB; ABA05500
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endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytolysis of a dendritic cell, inducing cytolysis of detecting the presence of a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a bacterium) to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat, autoimmune disease, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid perthritible sclerosis, diabetes mellitus, mysathenia gravis, pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves disease. The present sequence is that of the human monoclonal antibody B11 variable heavy chain, useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; loss agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 ileileTyrProGlyAspSerAspThrileTyrSerProSerPheGlnGlyGlnValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CGGGCGAGTCAGGGTATTAGCAGCTGG
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19
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31
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOLAN463-2A.SEQ (1-84) x AAM48005 (1-116)
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36.84%
33.33%
66.15%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing ecytotoxic T cell response in cancers and infectious diseases.

SEQ ID NO 4; 82pp; English

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) introduced beta human choronic gonadorropin (betafico), where the antibody comprises a heavy and/or light chain variable region derived from a human choronic gonadorropin, the sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847), or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are inned to betahog; (2) a molecular conjugate comprising a human shingle chain antibody that binds to human APCs linked to betahog; where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an activation antipent of the molecular conjugates of escribed above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cellmediated response against the antigen, (5) immunising a subject comprising doministering any of the molecular conjugates described above, which APCs such that the antigen, a cytokine which stimulatory agent; and priferation of endoritic cells and/or an immunostimulatory agent; and conjugate of the antigen and a monoclonal antibody which binde to APCs, and contacting the conjugate either in vivo or exvivo with APCs such that the antigen is internal sed, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate become against the antigen is internal sed, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate of the present eliciting a potent antigen specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present

Seguence 116 AA;

116 19 2 5 5 31 Matches: Conservative: Mismatches: Indels: Length: Gaps: 97.90 36.84% 33.33% 66.15% 0.0111 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

NOLAN463-2A.SEQ (1-84) x ADR46821 (1-116)

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50 ileileTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                       70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
                                                                                                                                                                                                                                            |||
90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106
                                                                                                                                                                                                           78
1 AICAICTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC-
                                                                                                                                                                                                              ----CGGGCGAGTCAGGGTATTAGCAGCTGG
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ADR46829 standard; protein; 411 AA.

ADR46829 ID ADR4 XX

ADR46829; 

18-NOV-2004 (first entry)

Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.

molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; pB11-betahCG molecular conjugate; fusion protein.

sapiens.

Synthetic.

WO2004074432-A2.

02-SEP-2004.

30-JAN-2004; 2004WO-US002725.

31-JAN-2003; 2003US-0443979P.

(MEDA-) MEDAREX INC.

Ramakrishna V; Keler T, Endres M, He L,

WPI; 2004-635555/61.

N-PSDB; ADR46828

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

Claim 16; SEQ ID NO 12; 82pp; English

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCS) linked to beta human chorionic gonadotropin (DetahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human chorionic gonadotropin (DetahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human composition of the man antibody heavy cast langate comprising a human antibody heavy chain antibody that binds to human APCs linked to betahCG, where the chain antibody that binds to human APCs linked to betahCG, where the conjugate comprising the single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprising on composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-comprising administering any of the molecular conjugates described above, with the antigen is simmunishing selecting and confidence of the molecular conjugates described above, with the antigen and a monoclonal antibody of the molecular conjugates grainst the antigen is internalised, processed and comprising or APCs, and contacting the conjugate either in vivo or exvivo with APCs such that the antigen and a monoclonal antibody with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate either in vivo or exvivo with APCs such that the antigen is internalised, processed and comprising a manner which induces or enhances a cytotoxic T cell response against the antigen. The moleculas conjugate either in vivo or exvivo with APCs such that the ant are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and CC VHS-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46649), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCS linked to betahCG, where the CC (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjust betahCG, comprising or enhancing a T cell-mediated immune response, against betahCG, comprising or enhancing any of the molecular conjugates corprised above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; in mediated response against the antigen; in modernally in combination with an adjuvant, a cytokine which stimulates conjugates described above, comprising deministering any of the molecular conjugates described above, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and compositions of the methods and can be used as a CDB agonist, contactic, antimicrobial, immunospitions of the present invention are vivous and in vaccines. The methods and compositions of the present invention. eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by invention.

Sequence 468 AA; 

468 119 23 31 Conservative: Mismatches: Indels: Length: Matches: Gaps: 97.90 36.84% 33.33% 66.15% 0.0168 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

x ADR46819 (1-468) NOLAN463-2A.SEQ (1-84)

ADR46827 standard; protein; 613 AA.

ADR46827;

(first entry) 18-NOV-2004

Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;

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The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (RPCS) intended to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human comprises a heavy and/or light chain, variable region derived from a human comprises of SEQ IO NV:15 germinal sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46447) or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain antibody that binds to human APCS linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates of secribed above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, gaints the antigen; is jumunishing a subject comprising administering any of the molecular conjugates described above with APCs such that the antigen is processed and presented to realization of dendritic cells and/or an immunostimulatory agent; and composition of the antigen and a monoclonal antibody which binds to APCs, and conjugate of the antigen and a monoclonal antibody which binds to APCs, and confucting the antigen is internalised, processed and (5) inducing to APCs, and confucting the conjugate either in vivo or exvivo with APCs such that the antigen is internalised, processed and compositions of the present invention article and antimalarial activities, and can be used as a cytocoxic or presented to reclise in a manner which induces or enhances a cytocoxic or corpusing action antigen action with APCs such that the antigen is internalised, pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing ecytotoxic T cell response in cancers and infectious diseases.
CD8 agonist, vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; betahCG-B11 molecular conjugate; fusion protein.
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N-PSDB; ADR46826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keler T, Endres M,
                                                                                                                                                                                                                                                                                                                                      WO2004074432-A2.
                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                  Synthetic
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613 2 2 5 31 Conservative: Mismatches: Indels: Length: Matches: 0.0182 97.90 36.84% 33.33% 66.15% Best Local Similarity: Sequence 613 AA; Percent Similarity: Alignment Scores: 

Query Match:

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The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present amino acid sequence represents the heavy chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
                                                                                                                                                            89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108
                                                                21
                                                                                         69 ileileTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                          Human phospholipase A2-specific monoclonal antibody heavy chain #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feng X;
                                                                                                                                                                                                                           109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
                                                                                                                                                                                                                                                                                                                                                                                                                       human, monoclonal antibody, phospholipase A2; PLA2;
inflammatory disorder; degenerative disorder;
joint inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; ast
Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
                                                                1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                            ------CGGGCGAGTCAGGGTATTAGCAGCTGG
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21
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3
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Matches:
Conservative:
Mismatches:
Indels:
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Gaps:
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                              NOLAN463-2A.SEQ (1-84) x ADR46827 (1-613)
                                                                                                                                                                                                                                                                                             ADP47114 standard; protein; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2003; 2003WO-US038234.
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(LEXI-) LEXICON GENETICS INC.
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67.65%
61.76%
65.00%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                           ADP47114;
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                                                                                                                                                                                                                                                            RESULT 8
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                                                                   RESULT 10
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                                                                 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                          antiinflammatory; immunomodulator; cytostatic; gene therapy
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                                                                                                                                                                                                                                                                              Anti-human PDGF-D antibody heavy chain protein sequence.
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Matches:
Conservative:
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                                                                                                          -----GCGAGTCAGGGTATTAGCAGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang X,
Gaps:
                        NOLAN463-2A.SEQ (1-84) x ADP47114 (1-118)
                                                                                                                                                                                            ADK18605 standard; protein; 129 AA
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Query Match:
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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Pred. No.:
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                                                                                                                                                                                                                        ADK18605;
                                                                                                                                                                  RESULT 9
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 306641880.0,99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
78
                                          -----ileSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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-----lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnfrp 83
                                                                                                                                                                                                                                                                                                                                      antiinflammatory; immunomodulator; cytostatic; gene therapy
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                                                                                                                                                                                                                                                                                      Anti-human PDGF-D antibody protein related sequence #17.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                          ADK18791 standard; protein; 129 AA.
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RESULT 11 ADK18895

1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60 

NOLAN463-2A.SEQ (1-84) x ADK18605 (1-129)

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Corvalan JRF,
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                            Homo sapiens
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                                                                                                                                                           Bezabeh B;
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DB:
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                                                                                                                                                                                                                       Weber R;
                                                                                                                                                                                                                                                                     New human monoclonal antibody that binds to platelet-derived (factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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                                                                             antiinflammatory; immunomodulator; cytostatic; gene therapy
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----IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp
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                                                          Anti-human PDGF-D antibody protein related sequence #121.
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Matches:
Conservative:
Mismatches:
Indels:
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ADK18895 standard; protein; 129 AA
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                                                                                                                                                                                                                       Jia X,
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                                                                                                                                                                                                   (ABGE-) ABGENIX INC
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Best Local Similarity:
                                                                                                                     WO2003057857-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 129 AA;
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Bezabeh B;
                                                                                                  Homo sapiens
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                                     06-MAY-2004
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                  ADK18895
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                           Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
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antiinflammatory; immunomodulator; cytostatic; gene therapy
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Matches:
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Best Local Similarity:
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The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of thibiting mesangial cell proliferation; and (4) a method of training mesangial cell proliferation; and (4) a method of traininflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mab) variable region sequence represents a human exemplification of the present invention.
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                                                                                                                                                                                                                                                                     Larochelle WJ, Lichenstein H;
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                                                                                                                                                                                                                                                                     Keyt B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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                                                                                                                                                                                                                                                                   Floege J, Gazit-Bornstein G,
                                                                                                                      16-SEP-2003; 2003WO-US029414.
                                                                                                                                                                16-SEP-2002; 2002US-0411137P.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADL25427
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                                      WO2004024098-A2
Homo sapiens.
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Pred. No.:
                                                                                25-MAR-2004
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Human anti-TNFa antibody light chain variable region SEQ ID NO:100

(first entry)

09-SEP-2004

ADP22194;

ADP22194 standard; protein; 116 AA

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human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antiinflammatory; antipsoriatic; antirheumatic; eating-disorder; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonis;

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The present invention describes a human monoclonal antibody (1) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22411); and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (S1, ADP22418) or (S4, ADP22424). Also described: (1) assaying (M1) the level of TNRa in a patient sample, comprising concacting with (T), and detecting the level of binding between the antibody and TNRa in fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (T); and (4) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of (T); and (4) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of (T); and (4) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of (T); and (A1) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of (T); and (T) inhibiting (M3) TNRa induced apoptosis antihinflammatory, antipocratic, antitheumatory, antipocratic, antitheumatory, antipocratic, antitheumatory, antipocratic, antitheumatory, antipocratic, antitheumatory, antipocratic, cancer, ovarian cancer, bidder cancer, colon cancer, ovarian cancer, bladder cancer, colon cancer, and prostrate cancer, kidney cancer, colon cancer, ovarian cancer, bladder cancer, colon cancer, ovarian cancer, bladder cancer, colon cancer, and prostrate cancer, solon cancer, colon cancer, and prostrate cancer, solon cancer, colon cancer, ovarian cancer, bladder cancer, colon cancer, and prostrate cancer, solon cancer, and prostrate cancer, solon ca
induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
                                                                                                                                           rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reaction, septic shock, cachexia, anorexia, multiple sclerosis.
                              bladder cancer; lung cancer; glioblastoma; stomach cancer; endometrial cancer; kidney cancer; colon cancer; prostrate cancer; immuno-mediated inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
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Conservative:
Mismatches:
Indels:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; monoclonal antibody; phospholipase A2; PLA2; inflammatory disorder; degenerative disorder; disorder; doint inflammatory reaction; skin inflammatory reaction; blood vessels inflammatory reaction; arthritis; psoriasis; asthma; Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
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90 AspThrAlaMetTyrTyrCysAlaArgSerGlyTyrGlyMetAspValTrp 106
                                                                                                                                                                                                                                                                                                                                                                    -----CGGGCGAGTCAGGGTATTAGCAGCTGG
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Matches:
Gaps:
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                                                         NOLAN463-2A.SEQ (1-84) x ADP22194 (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP47088 standard; protein; 118 AA.
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Jia X, Nocerini MR;
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(LEXI-) LEXICON GENETICS INC.
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Conservative: Mismatches: Indels:

Percent Similarity: Best Local Similarity: Query Match:

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50 IlelleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                                                                                                  70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
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                                                          1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCG---
                                                                                                                                                                                                                                                                                                                                 90 AspThrAlaMetTyrTyrCysAlaArgHisTrpSerTyrGlyMetAspValTrp 107
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NOLAN463-2A.SEQ (1-84) x ADP47088 (1-118)
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Sequence 33, Application US/08665202
| Patent No. 5977322
| GENERAL INFORMATION:
| APPLICANT: Marks, James D. | APPLICANT: Schier, Robert |
| TITLE OF INVENTION: Tumor Antigens | TITLE OF INVENTION: Tumor Antigens |
| VOMBER OF SEQUENCES: 141 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP |
| STREET: Two Embarcadero Center, Eighth Floor |
| CONTEST California |
| COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION 3-424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPLICATION NUMBER: US 60/000,250
US-09-490-153-40

US-09-490-324-67

US-09-490-324-67

US-08-490-324-67

US-08-665-202-46

US-08-665-202-53

US-08-665-202-54

US-08-665-202-44

US-08-665-202-45

US-09-315-574-53

US-09-315-574-54

US-08-665-202-49

US-08-665-202-49

US-08-665-202-49

US-08-665-202-55

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US-08-665-202-57

US-08-665-202-57

US-08-665-202-57

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US-09-315-574-44

US-09-315-574-45

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US-09-315-574-45
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US-09-315-574-57
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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
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 RESULT 1
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                                                                           ; Search time 22.25 Seconds (without alignments) 563.642 Million cell updates/sec
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/cgn2_6/ptGdata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptGdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptGdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptGdata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptGdata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                      protein search, using frame_plus_n2p model
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US-09-315-574-33
US-09-726-219A-171
US-08-545-809A-133
US-09-025-769B-26
US-09-490-153-26
US-09-025-769B-40
US-09-025-769B-67
US-09-025-769B-67
US-09-025-769B-67
US-09-025-769B-67
US-09-490-070A-40
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             2005, 18:44:26
                                                                                                                                                                              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
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                                                                                                                        NOLAN463-2A.SEQ
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Query Match:
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Patent No. 612097
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF INVENTION:
COURTESPONDENCE:
CORRESPONDENCES:
CORRESPONDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
CITY: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                           283228
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION WUNBER: 38.498
REFERENCE, DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPRAM: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UNN-1995
FILING DATE: 14-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UNN-1995
PRIOR APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UNN-1996
ATTORNEY/AGENT INFORWATION:
                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ 1D NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-33
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                0.00843
92.20
67.65%
58.82%
62.30%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-09-315-574-33
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y APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Winter, Timochy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT APPLICATION NUMBER: US 9015198.6
FRIOR PRING DATE: 1990-07-10
FRIOR APPLICATION NUMBER: GB 9012845.3
FRIOR PILING DATE: 1990-10-10
FRIOR PILING DATE: 1990-10-10
FRIOR APPLICATION NUMBER: GB 902845.3
FRIOR APPLICATION NUMBER: GB 902453.6
FRIOR APPLICATION NUMBER: GB 90450-10-10
FRIOR APPLICATION NUMBER: GB 910474.9
FRIOR FILING DATE: 1991-03-06
FRIOR PILING DATE: 1991-03-06
FRIOR FILING DATE: 1991-03-01-08
FRIOR FILING DATE: 1993-01-08
FRIOR FILING DATE: 1995-06-07
FRIOR FILING DATE:
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Conservative:
Mismatches:
Indels:
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APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOLAN463-2A.SEQ (1-84) x US-09-315-574-33 (1-98)
                                                                                                                                                                                                                                                                                                                                  Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 171, Application US/09726219A; Patent No. 6806079; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pope, Anthony
Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
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Chiswell, David
                                                                                                                                                                                                                                                                                                                              0.00843
92.20
67.65%
58.82%
62.30%
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Holliger, Kasper
Marks, James
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-726-219A-171
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COUNTRY: ....

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM RYEB. Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM NUMBER: IBM COMPONER

COMPUTER: IBM PC compatible

COMPUTER: IBM PC c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                           ||| ::: ||||||:::
89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 102
                                                                                                                                                              78
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OP SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                           55 -----GCGAGTCAGGGTATTAGCAGC-----TGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
          NOLAN463-2A.SEQ (1-84) x US-08-545-809A-133 (1-117)
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US-09-205-769B-26
Sequence 26, Application US/09025769B
; Patent No. 6300064
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amino acid
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STATE: New York
COUNTRY: USA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 133, Application US/08545809A

Fatent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STATE: MA

COUNTRY: US

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                  1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG-
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20
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MEDIUM TYPE: Disketter
COMPUTER: Disketter
APPLICATION NUMBER: Disketter
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05501/004001
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                NOLAN463-2A.SEQ (1-84) x US-09-726-219A-171 (1-111)
                                                                                                                                                                                                                                     Gaps:
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INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
                                                                                                       0.00879
                                                                                                                            92.20
67.65%
58.82%
62.30%
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; ORGANISM: Homo sapiens
US-09-726-219A-171
                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-08-545-809A-133
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                                                                       Alignment Scores:
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Pred. No.:
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No.:
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ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PetentIn Release #1.0, Version #1.30 (BPO)
SOFTWARE: PetentIn Release #1.0, Version #1.30 (BPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
PRICHATION NUMBER: US/09/490,070A
FILING DATE: 18-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 37629-0005
TELECOMMUNICATION NUMBER: 37629-0005
TELECOMMUNICATION OF SEQUENCE THANKER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 -----GCGAGTCAGGGTATTAGCAGC------TGG 78
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
ULE TYPE: protein
ENCE DESCRIPTION: SEQ ID NO: 26:
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                                                                                                 Sequence 26, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
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US-02-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
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67.65$
58.82$
62.30$
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STATE: D.C.
COUNTRY: USA
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Best Local Similarity:
Query Match:
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SEQUENCE
US-09-490-070A-26
                                                      RESULT 6
US-09-490-070A-26
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COMPUTER: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
CORENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION MUNBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Janes F. Haley, Jr., Esq.
REGISTRATION UNMBER: 27,794
REGISTRATION UNMBER: 27,794
REGISTRATION NUMBER: AMPRICATION:
TELECOMMUNICATION: (212)596-9000
                                                                                                                                                                                               c/o Fish & Neave
GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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Matches:
Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26
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; Sequence 26, Application US/09490324
; Patent No. 6826422
; GENERAL INFORMATION:
; APPLICANT: Pack, Peter
; Ilag, Vic
; Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acida
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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92.20
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58.82%
62.30%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-09-490-324-26
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1 ATCATCTATCCTGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG--
                                                                                                                                                                                       SOFTWARE: PATENTIN STAIRS
CURRENT APPLICATION DATA: PC. DOS/NOS-LOS
CURRENT APPLICATION DATA: PC. DOS POST STAIRS
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: BP 95 11 3021.0
PRIOR APPLICATION NUMBER: BP 95 11 3021.0
APPLICATION NUMBER: BP 95 12 3021.0
ATTORNEY AGENT INFORMATION: NAME: James F. Haley, Jr., Esq.
REJECTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
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APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
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Matches:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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; Patent No. 6300064
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ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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67.65%
58.82%
62.30%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                       New York
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Best Local Similarity:
Query Match:
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STATE: New York
COUNTRY: USA
                                                                              USA
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ADDRESSEE:
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US-09-025-769B-67
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                                                                            COUNTRY:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
FILING DATE: A-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG-
                                                                                    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
              Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; STRANDENESS: <URNown>; STRANDENESS: <Unknown>; TOPOLOGY: linear; MOLECULE TYPE: protein SEQ ID NO: 26: US-09-490-324-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-025-769B-40; Sequence 40, Application US/09025769B; Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knappik, Achim
Pack, Peter
Ilag, Vic
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92.20
67.65%
58.82%
62.30%
                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR
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RESULT 12
US-09-490-070A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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Sequence 40, Application US/09490070A

Sequence 40, Application US/09490070A

Sequence 40, Application US/09490070A

Sequence 40, Application US/09490070A

GENERAL INFORMATION:

Pack, Peter

I pack
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1995
FILING DATE: 18-MG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE JAMES PROCKET NUMBER: 27,794
REFERENCE TO NINFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
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Indels:
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amino acid
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Best Local Similarity:
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Sequence 67, Application US/09490070A

Sequence 67, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPENDENCE ADDRESS:
MUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:
MADRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
Mine & Madre & Ma
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REDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 912-200
TELEFAX: (202) 912-202
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: cUnknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOLAN463-2A.SEQ (1-84) x US-09-490-070A-40 (1-120)
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REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
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STATE: D.C.
COUNTRY: USA
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67.65$
58.82$
62.30$
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Best Local Similarity:
Query Match:
DB:
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STRANDEDNESS: <Unknown>
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US-09-490-153-40
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                                                                                                                                                                                                                                                                                                                     55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78
                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                            INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTIS:
LENGTH: 120 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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(202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
TELEPRA: (212)596-9000
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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92.20
67.65%
58.82%
62.30%
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Best Local Similarity:
Query Match:
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US-09-490-153-40
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50 IlelleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
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CONDUTE: New York
COUNTY: USA
ZIP: 10021
COMPUTE: READABLE FORM:
MEDIUM TYPE: PLOPBY disk
COMPUTE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
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Matches:
Conservative:
Mismatches:
Indels:
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REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
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Best Local Similarity:
Query Match:
DB:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BFO)
CURRENT APPLICATION NUMBER: US/09/490,324
FLING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FLING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FLILNG DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/09490324
; Patent No. 6828422
; Patent No. Forter Tlag, Vic Ge, Liming Moroney, Simon Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
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Conservative:
Mismatches:
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: WORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
EMPERAY: (212) 596-9000
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-324-40
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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67.65%
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62.30%
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Query Match:
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Alignment Scores:
Pred. No.:
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US-09-490-324-40
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Search completed: August 4, 2005, 19:04:14 Job time: 25.25 secs

Perfect score:

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Scoring table:

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; Publication No. US20030167502A1
; GENERAL INFORMATION:
APPLICANT: Boo' Yashwant M.
APPLICANT: Keler, Tibor
; ITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MX1-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR PILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR PELING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-769-144-12

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US-10-769-144-12

US-10-041-860-25

US-10-041-860-25

US-10-041-860-25

US-10-041-860-25

US-10-763-332-3

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US-10-76-332-3

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SUMMARIES
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Match
                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                    August 4, 2005, 19:01:38; Search time 78.75 Seconds (without alignments) 832.849 Million cell updates/sec
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                                                                                                                                                                84
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database :

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                                                                                                                            APPLICANT: Keler, Tibor
APPLICANT: Keler, Tibor
APPLICANT: Keler, Tibor
APPLICANT: Renexishina, Venky
TITLE OF INVENTION: THEREFOR
THEREFOR TELLING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR PLILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 4
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APPLICANT: Relet, Tibor
APPLICANT: Bndres, Michael
APPLICANT: Branckishna, Venky
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES;
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/10/769,144
CURRENT APPLICATION NUMBER: 60/443979
PRIOR PILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
                                                                     Sequence 4, Application US/10769144; Publication No. US20040248215A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.90
36.84%
33.33%
66.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ACIE, Tachwant M.
APPLICANT: ACIE, Tibor
TITLE OF INVENTION: CELLS
CURRENT APPLICATION UNMER: US/10/035,637
CURRENT APPLICATION UNMER: US/80,637
CURRENT APPLICATION NUMBER: USSN 60/203,126
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FaatSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CGGGCGAGTCAGGGTATTAGCAGCTGG 78
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Matches:
Conservative:
Mismatches:
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Matches:
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US-10-035-637-4
                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
                                              ; ORGANISM: HC
US-09-851-614-4
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US-10-035-637-4
     LENGTH: 116
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Endres, Michael
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|231 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 247
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                                                                                                                              1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC---
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                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10769144

Publication No. US20040248215A1

GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Remackrishna, Venky
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MXI-301
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US/10/769,144
CURRENT FILING DATE: 2004-01-30
PRIOR PILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTHARE: FastsEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 468
 411
19
2
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31
1
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119
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
0.0236
97.90
36.84%
33.33%
66.15%
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97.90
36.84%
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66.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 -----
                        Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
DB:
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Pred. No.:
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89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108
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Sequence 29, Application US/10726332

Publication No. US20050058649A1

GENERAL INFORMATION:

APPLICANT: Gregory M. Landes

APPLICANT: Ling Chen

APPLICANT: Ling Chen

APPLICANT: Meina Linng

APPLICANT: Mark R. Nocerini

ITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2

ITLE OF INVENTION: AND USES THEREOF

FILE REPERENCE: ABGENIX.072A

CURRENT APPLICATION NUMBER: US/10/726,332

CURRENT FILING DATE: 2003-12-02

PRIOR FILING DATE:

PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
APPLICANT: He, Lizhen
APPLICANT: Ramakrishna, Venky
TITLE OF INVENTION: THEREOR VACCINE CONJUGATES AND USES;
TITLE OF INVENTION: THEREOR
FILE REFERENCE: MXI-301
CURRENT PEPLICATION NUMBER: US/10/769,144
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR PILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 613
TWOED: NOTE
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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SOFTWARE: FastSEQ for Windows Version 4.0
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97.90
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96.20
67.65%
61.76%
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; ORGANISM: Homo sapiens
US-10-769-144-10
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US-10-726-332-29
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-726-332-29
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LENGTH: 118
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RESULT 10
US-10-041-860-250
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                                                                                                         ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG-----
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Sequence 29, Application US/10041860

Publication No. US20303157109A1

Sequence 29, Application US/10041860

Publication No. US20303157109A1

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Fend, Xiao-Chi

APPLICANT: Fend, Xiao-Chi

APPLICANT: Pend, Xiao-Dong

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Weber, Saracine

APPLICANT: Weber, Saracine

APPLICANT: Weber, Solary

APPLICANT: Weber, Solary

APPLICANT: Weber, Solary

APPLICANT: ANTIBODIES DIRECTED TO PDGFD AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29

TYPE: PRT

CREANISM: homo sapiens

US-10-041-860-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 215, Application US/10041860
; Publication No. US20030157109A1
GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.;
APPLICANT: Feng, Xiao-Chi
; APPLICANT: Feng, Xiao-Chi
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Gazit, Gadi
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                  55 -----GCGAGTCAGGGTATTAGCAGC------TGG 78
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Matches:
Conservative:
Mismatches:
Indels:
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                                                     NOLAN463-2A.SEQ (1-84) x US-10-726-332-29 (1-118)
Indels:
Gaps:
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57.50%
50.00%
64.46%
 65.00%
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Best Local Similarity:
Query Match:
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US-10-041-860-215
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1 ATCATCTATCCTGGTGACTCTGATACCCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
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70 -----lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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APPLICANT: COLVAIAN, JOSE R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 250
LENTH: 129
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                      NOLAN463-2A.SEQ (1-84) x US-10-041-860-215 (1-129)
CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 215 LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 250, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGGGTATTAGCAGC----
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CORGANISM: homo sapiens
US-10-041-860-250
                                                                                                              r TYPE: PRT
CORGANISM: homo sapiens
US-10-041-860-215
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                                                                                                                             APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 319
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Publication No. US20040141969A1

GENERAL INFORMATION:

APPLICANT: Floege, Juergen

APPLICANT: Keyt, Bruce

APPLICANT: LaRochelle, Henri

APPLICANT: Lichentein, Henri

TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS

TITLE OF INVENTION: WEING ANTI-PDGF-DD ANTIBODIES

FILE REFERENCE: ABGENIX.052A

CURRENT APPLICATION NUMBER: US/10/665,383

CURRENT FILING DATE: 2003-09-16

PRIOR FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 129
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            Application US/10041860
5. US20030157109A1
                           Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yeng, Xiao
APPLICANT: Chen, Kiao-Dong
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ORGANISM: homo mapienm
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; ORGANISM: homo sapiens
US-10-665-383-38
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US-10-665-383-38
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50 ileileTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: PACTOR AND USES THEREOF
FILE REFERENCE: AGGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR APPLICATION NUMBER: 60/430729
PRIOR APPLICATION NUMBER: 60/430729
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                                                       NOLAN463-2A.SEQ (1-84) x US-10-665-383-38 (1-129)
Indels:
Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
                                                                                                                                                                                                                                                                                   , Sequence 100, Application US/10727155
, Publication No. US20050049402A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mary Haak-Frendscho
Palaniswami Rathanaswami
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US-10-726-332-3
; Sequence 3, Application US/10726332
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Kathy Manchulencho
Raffaella Faggioni
Giorgio Senaldi
                                                                                                                                                                    61 CAGGGTATTAGCAGC---
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APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Scott Klakamp
64.46%
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Meina Liang
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ORGANISM: Homo sapiens
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US-10-726-332-5
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; Sequence 5, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Ling Chen
; APPLICANT: Ling Chen
; APPLICANT: Meina Liang
; APPLICANT: Xiao-Fani
; APPLICANT: Xiao-Fani
; APPLICANT: Xiao-Fani
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: 2003-12-02
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 118
## Publication No. US20050058649A1
| GENERAL INFORMATION: |
| JAPPLICANT: Gregory M. Landes |
| APPLICANT: Gregory M. Landes |
| APPLICANT: Ling Chen |
| APPLICANT: Wary Haak-Frendscho |
| APPLICANT: Xiao Feng |
| APPLICANT: Xiao Feng |
| APPLICANT: Xiao Feng |
| APPLICANT: Xiao Chi Jiao |
| APPLICANT: Alao Chi Jiao |
| APPLICANT: Alao Chi Jiao |
| TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 |
| TITLE OF INVENTION: AND USES THEREOF |
| FILE REFERENCE: ABGENIX.072A |
| FILE REFERENCE: ABGENIX.072A |
| CURRENT APPLICATION NUMBER: US/10/726,332 |
| PRIOR APPLICATION NUMBER: n/a |
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ORGANISM: Homo sapiens
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US-10-726-332-5
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Ig heavy chain V region (clone PBL12) - human (fragment)

Cipecies: Homo sapiens (man)
Cipecies: Homo sapiens (man)
Cipate: 30-8ep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
Cipate: 30-8ep-1993 #sequence_revision of a rearranged VH5 gene in human B ce A; Reference number: PH1231, MUID:93018822; PMID:1402653
A; Reference number: PH1232; MUID:93018822; PMID:1402653
A; Residues: 1-102 < CAI-
A; Residues: 1-103 < CAI-
A; Residues: 1-103 < CAI-
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                               PH1280
PH1258
PH1273
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PH158
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PH1559
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PH1410
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PH1410
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S12580
PH1265
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61 CAGGGTATTAGCA
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|ThrileLeuAla
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Percent Similarity:
Best Local Similarity:
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OMOBELETARE A. 12P. model - DEVEXIP

O= / Cgn2 1/USFTO spool p/NOLAN08728463-2/runat_04082005_123944_22592/app_query.fasta_1.5

O= / Cgn2 1/USFTO spool p/NOLAN08728463-2/runat_04082005_123944_22592/app_query.fasta_1.5

OBS-PIR - OFFITE as prod_1 p/NOLAN08728463-2/runat_040.1 - LOOPCL=0 - LOOPEXT=0

- UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45

- DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_NIN=0 - ALIGN=15 - MODE=LOCAL

- OUTFWT=ptc - NORM=ext - HEAPSIZE=500 - MNINEN=0 - MAXLEN=200000000

- USER=NOLAN08728463-2 - GCGN 1 1 77 - QTUNAT - DSPBLOCK=100 - LOOPCEX - ICPU=3

- UND WMAP - LARGEQUERY - THE SCORES=0 - WAITT - DSPBLOCK=100 - LOOPCEX - ICPU=3

- NO WMAP - LARGEQUERY - THE START - LARGEDOR - LOOPCEX - ICPU=3

- FGAPEXT=0.1 - YGAPOP=10 - YGAPEXT=0.1 - DELOP=6 - DELEXT=0.1
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                                                                                                 4, 2005, 18:42:17; Search time 17.75 Seconds (without alignments) 910.671 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                         1 ATCATCTATCCTGGTGACTC.....GTATTAGCAGCTGGTTAGCC
           version 5.1.6
- 2005 Compugen Ltd.
                                                                      OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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PH1409
PH1414
C36006
PH0877
PH1274
S26907
S12424
PH1266
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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              GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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pir2:*
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Match
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12243044654321

Score

Result

Database :

cell chror

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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession. C36006
C;Accession. C36006
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36006
A;Status: preliminary
                                                                                                                                                                                         response: High incidence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (clone P1-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: FH1414
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High in dermatitis.
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                                                                                                                                                                                                                                                                                                                                                                                  Met
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C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Superferences:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;Is-98/Domain: immunoglobulin homology <IMM>
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70 IleSerAlaAspGluSerIleSerThrAlaTyrLeuGlnTrp 83
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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Ig heavy chain V region (83p2) - human
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A;Residues: 1-123 <SCH>
A;Cross-references: GB:M34022
                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-127 <VAN>
A,Experimental source: PBMC
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Ig heavy chain V region (clone CORD7) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 10-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1249
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B ce A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1249
A;Residues: 1-102 <AIN-A;Residues: 1-102 <AIN-A;Residues: 1-102 <AIN-A;Residues: I-102 <AIN-A;Residues: I-103 <AI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 03-reb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C; Accesion: PH409
R; van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A; Title: Molecular evolution of the human immunoglobulin E response: High in A; Reference number: PH1409; MUID:93115676; PMID:8418213
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A;Molecule type: mRNA
A;Residues: 1-127 < VANA
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology < IMM>
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Matches:
Conservative:
Mismatches:
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95.60
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72 |ThrileLeuAla 76
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Ig heavy chain V region (DP-73) - human (Species: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pecies: Homo sapiens (man) (5.5pecies: Homo 22.6Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 (5.5peciesion: 826607 (7.5peciesion: 1.M.; Malter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. Nol. Biol. 227, 776-778, 1982 (7.5peciesion: Malter, G. Marks, J.D.; Llewelyn, M.B.; Winter, G. A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Reference number: $26885; MUID:93021117; PMID:1404388
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C; Specias: Homo sapiens (man)
C; Date: 18-Feb-1994 #sequence revision 10-Nov-1995 #text_change 03-Aug-1998
C; Accession: S12424; S12425; S12426; S12427; S12429; S12432
R; Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; MUID:90059975; PMID:2511001
                                    A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12373; NID:g32965; PIDN:CAA78243.1; PID:g32966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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A;Cross-references: EMBL:X56373
A;Accession: S12426
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A;Residues: 1-101 <SA3>
A;Cross-references: BMBL:X56370
A;Accession: S12427
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A; Status: translation not shown
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Best Local Similarity:
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C;Species: Homo sapiens (man)
C;Species: Office-Institute (manual transfer of the same of t
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                                                           70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
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C'Species: Homo sapiens (man)
C'Accession: PH1274
R'Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A; Fitle: Extensive and selective mutation of a rearranged VH5 gene in human A; Reference number: PH1232; MUID: 93018822; PMID: 1402653
A; Rocession: PH1232; MUID: 93018822; PMID: 1402653
C'Subscriments Hource: adult PBL
C'Suberfamily: immunoglobulin V region; immunoglobulin homology
C'Superfamily: immunoglobulin
                                                                                                                                                                                    90 AspThrAlaMetTyrTyrCysAlaArgHisAsnSerGlnThrGlyAlaSerLeuTrp 108
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C;Species: Homo sapiens (man)
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Conservative:
Mismatches:
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46.15$
62.43$
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Best Local Similarity:
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Pred. No.:
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To have year thain V region (clones CLill, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD-1

C; Species: Howo sapiens (man)

C; Species: How PH1279

R; Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

R; Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

A; Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron A; Reference number: PH1232; MUID:93018822; PMID:1402653

A; Accession: PH1279

A; Rescidues: 1-102 < CAI-

A; Rescidues: 1-102 < CAI-

A; Rescidues: adult PBL

C; Superrimental source: immunoglobulin

F; 19-102/Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J: Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87
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A; Residues: 1-102 < CAI>
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A;Status: translation not shown
A;Rolecule type: DNA
A;Residues: 1-101 <8A4>
A;Cross-references: EMBL:X56368
A;Accession: $12429
A;Accession: $12429
A;Residues: 1-101 <8A5>
A;Residues: 1-101 <8A5>
A;Residues: 1-101 <8A5>
A;Cross-references: EMBL:X56369
A;Accession: $12432
A;Cross-references: EMBL:X56369
A;Accession: BNA
A;Residues: 1-101 <8A5>
A;Cross-references: EMBL:X56371
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>
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74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp
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Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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Ig heavy chain V region (clone CORD2) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 30 - Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-2
C; Accession: PH1244
R; Cai, J; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A; Title: Extensive and selective mutation of a rearranged VH5 gene. A; Reference number: PH1232; MUID: 93018822; PMID: 1402653
A; Accession: PH1234
A; Molecule type: DNA
A; Residues: 1-102 - CAI>
A; Experimental source: cord blood B cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 19-102/ Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
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C;Accession: PH1202
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MUBDLINE=97450619; PubMed=9107060; DOI=10.1016/S0161-5890(97)00042-4;
MUBDLINE=97450619; PubMed=9107060; DOI=10.1016/S0161-5890(97)00042-4;
MUBDLINE=97450619; Glannoni M.A.; Hartman S.L.; Elliott E.A.; Squinto S.P.;
Mutler L.A., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric 19G2/G4 constant regions block human leukocyte binding to porcine endothelial cells.";
"A.441-452(1997).
                                                                                                                                                                                                                                                                                                   Q9ZIC4;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-pordine VCAM mAb 3F4 heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                 usa musculus (Moubse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; U78801; AAD00293.1; -.
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      version 5.1.6
- 2005 Compugen Ltd.
                                        protein search, using frame_plus_n2p model
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Copyright (c) 1993
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
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                                                      4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG 63
                                                                                                                    69
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                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700110111 product:immunoglobulin heavy chain of (heavy
mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
The FANTOM Consortium,
the FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation (60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CSTBL/6J; TISSUE-Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Fonda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN-CS-BL/6J; TISSUE-Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                      111 AA
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                      PRT;
NOLAN463-2A.SEQ (1-84) x Q9Z1C4 (1-118)
                                                                                                                                                                           64 GGTATTAGCAGCT 76
                                                                                                                                                                                                                     ----LeuThrAla 72
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                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    Q9D9B8;
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ATTACHENCE FORM N. A. T. STUEE-Manmary tumoc;

STRAILE-CZECH II. TISSUE-Manmary tumoc;

REDINE-2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hatch F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Macusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carnino; P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Schards S.A., McEwan P.J., McKerman K.J., Malek J.A., Gubbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse CDNA sequences.";
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T., Muramatsu M., Hayashizaki Y., Suzuki H., Yoshino M., Muramateu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                               111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;
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13
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                        EMBL; AK007163; BAB24877.1; -. HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 111 AA; 11976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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68.30
58.62%
44.83%
46.15%
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Best Local Similarity:
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Query Match:
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TISSUE—Primary B-Cells;

RA TISSUE—Primary B-Cells;

RA MILEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA STEAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteshul S.F., Zeeberg B., Buetow K.H., Schemfer C.F., Bhat N.K.,

RA Alteshul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh P.,

RA Stapleton M.J., Usdin T.B., Toohiyuki S.I., Wang J., Heiseh P.,

RA Stapleton M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C.,

RA Boask S.A., McEwan P.J., McKernan K.J., Malley S.J.,

RA BOASK S.A., McEwan P.J., Wnokrernan R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Kettemen M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG 63
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                   MGD; MGG:2144967; AU044919.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-8et; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00395; IG_MHC; UNKNOWN_1.
PROSITE; PS00395; IG_MHC; UNKNOWN_1.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                         Strausberg R.; Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC025447; AAH25447.1; -. HSSP; P01865; ICL7.
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14
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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Indels:
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                                          SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Mammary tumor;
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----LeuThrAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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OGGMX8

OGGMX8

AC OGGMG

AC OGGMG

DT 05-JI

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MEDLINE-218B.57; PubMed=1247793; DOI=10.1073/pnas.242603899;
NEDLINE-218B.257; PubMed=1247793; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Doitchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Experten M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Wyers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
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17 PheProGlySerArgCysAspIleGlnMetThrGlnSerProSerSerValSerAlaSer 36
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                    Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BEO73764; ARH73764.1; -
InterPro; IPR005599; IG.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
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18
1
7
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2
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC60843 protein.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF07654; C1-8et; 1.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS0290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                            InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
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                                                                                                                       IISSUE=Primary B-Cells;
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                                                                                            SEQUENCE FROM N.A.
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Best Local Similarity:
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26 ArgThrGlyCysSerTrpPheLyslleLeuLeuDheTyrValllePheTyrGlyCysLeu 45
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                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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MEDLINE-83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion.";
GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; NAS. GO; GO:0006813; P:potassium ion transport; NAS. GO; GO:0006814; P:sodium ion transport; NAS. InterPro; IPR000402; Na/K_ATPase_beta. PEfam; PF00287; Na K-ATPase_bet; 1. TIGRFAMS; TIGR01107; Na K-ATPase_bet; 1. PROSITE; PS00390; ATPASE NA K BETA 1; 1. PROSITE; PS00391; ATPASE NA K BETA 2; 1. PROSITE; PS00391; ATPASE NA K BETA 2; 1. TRANSMEMDIANE.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-81098966; PubMed-6779204;
Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
115 Kappa chain V. I region HK101 precursor (Fragment).
Homo sapiens (Human).
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Matches:
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Mismatches:
Indels:
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174
274
263
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Best Local Similarity:
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P01601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 15, Last sequence update)
Sodium/potassium-ransporting Afpase beta-233 chain (Sodium/potassium-ransporting Afpase beta-233 chain (Sodium/potassium-ransporting Afpase beta-233 subunit).
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Am. J. Physiol. 279:R222-R229(2000).
-!- FUNCTION: This is the non-catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of Na (+) and K(+) ions across the plassma membrane.
-!- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
               Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anguilla anguilla (European freshwater eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
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-!- TISSUE SPECIFICITY: Expressed mainly in epithelial tissues.
-!- SIMILARITY: Belongs to the Na+/K+ and H+/K+ ATPases beta chain
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b; AJ239317; CAB85586.1; -.
GO:0005890; C:sodium:potassium-exchanging ATPase complex; NAS.
                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053409; AAH53409.1; -.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
Pfam; PF07654; C1-set; 4.
SWART; SW00406; IGV.
PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;
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112
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                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                     STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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67.30
58.62%
41.38%
45.47%
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                                                                        and mouse cDNA sequences.
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                                                                                                                                                             SEQUENCE FROM N.A.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 AlaSerValGlyAspArgValThrIleThrCysArgAlaArgGlnGlyIleSerTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCATCTATCCTGGT-----GACTCTGATACCACATACAGCCCGTCC--
                                                                                                                                                                                                                                                                                   kappa chain V-I region HK101.
                                                                                                                                                                                                                                                                                                   Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                              Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                   12799 MW; D7D0FF3718CEF587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human):
                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 236 AA
                                                                                                                                                                                                                                                                                                                                                              similarity
                                                                                                        EMBL; K01322; AAA58930.1; -.
EMBL; K01324; AAA58932.1; -.
EMBL; V0058; CAA23824.1; -.
FIR; A01881; KHU11.
HSSP; P01607; IBWW.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                         Framework-3.
                                                                                                                                                                                                                                                                                Ig kappa cha
Framework-1.
                                                                                                                                                                                                                                                                                                                   Framework-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOLAN463-2A.SEQ (1-84) x KV11_HUMAN (1-117)
                                                                                                                                                                                                                       Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                    86
63.60
45.24
40.48
42.97
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                                                                                                                                                                                                                                                                                                                                       110
×117
110
Cell 32:181-189(1983).
                                                                                                                                                                                                                                                                                                                                                                                  117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAGCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAla 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                             DOMAIN
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06PIH7
1D 06PIH7
AC 06PIH7
DT 05-J
DT 05-J
DD 05-J
DD Hypo
DD Hypo
OC BUKA
OC MARM
OX NCBI
RN [1]
RN [1]
RN SEQU
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rausberg R.L., Feingold E.A., Grouse L.H., Dorge J.G., Rausberg R.L., Caceberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Romantein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKwan P.J., McKernan K.J., Mallek J.A., Gunzarene P.H., M. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Jones S.J., Marra M.A., Saliska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Ander M., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Salaka M., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 ProdlyAlaArgCysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerVal 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 GlyAspArgValThrIleThrCysArgAlaSerGInGlyIleSerSerTyrLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Straubberg R.;
L Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

R SMBL; BC034141; AAH34141.1; -.
R HSSP; P01607; 1AR2.
R InterPro; IPR001599; Ig.
R InterPro; IPR001596; Ig.
R InterPro; IPR001506; Ig.
R R SMART; SM00409; IG. 2.
SMART; SM00409; IG. 1.
SMART; SM00409; IG. 1.
R SMART; SM00409; IG. 1.
SMART; SM00409; IG. 1.
SMART; SM00409; IG. 1.
R PROSITE; PS00290; IG. MKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Created).
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOLAN463-2A.SEQ (1-84) x Q6PIH7 (1-236)
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63.60
48.72
46.15
42.97
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Alignment Scores:
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DOMAIN
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DISULFID
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SEQUENCE
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                                                                                                                                    Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                     1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2; Yancopoulos G.D., Alt F.W.; "Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region VH558 A1/A4. Framework-1.
                                 Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-1.
                                                                                                                                     473 AA; 53210 MW; 6F8197395A1C7F79 CRC64;
                                                                                                                                                                     473
13
4
6
6
15
                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    117 AA
                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                 61 CAGGGTATTAGCAGCTGGTTAGCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JASP; Put.
InterPro; IPR003596,
InterPro; IPR003596,
Pfam; PF00047; ig; 1.
A SMART; SM00406; IGv; 1.
JR PROSITE; PS50835; IG LIKE; 1.
TRMNLOGlobulin V region; Signal.
1 TGNAL 20 117 IG h
20 117 IG h
20 17 IG h
20 549 Fra
                                                                          EMBL; AAABO1008980; EAA14419.1; -.
Interpro; IPR005654; AFG1_ATPase.
Pfam; PF03969; AFG1_ATPase; 1.
                                                                                                                                                                                                                                                  NOLAN463-2A.SEQ (1-84) x Q7Q1B6 (1-473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M13787; AAA38499.1; -. PIR; AO2029; HVMSA1. HSSP; P01820; 1G7J. InterPro; IPR007110; IG-like. InterPro; IPR003596; IG_V.
                                                                                                                                                                     111
63.50
44.74%
34.21%
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                        Best Local Similarity:
             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                    HV52 MOUSE
                                                                                                                                     SEQUENCE
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Meliceae; Glyceria.
                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
          Complementarity-determining-2.
                                                 12971 MW; 8B0BC138856DFC9D CRC64;
                                                                            1117
112
4
6
7
                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                               436 AA
                              By similarity.
                                                                            Length:
Matches:
  Framework-2.
                     Framework-3
                                                                                                                            Gaps:
                                                                                                                                               NOLAN463-2A.SEQ (1-84) x HV52_MOUSE (1-117)
                                                                                                                                                                                                                                                               PRT;
                                                                                     62.30
55.17$
41.38$
42.09$
                                                                                                                                                                                                      64 GGTATTAGCAGCT 76
                                                                                                                                                                                                                        ----LeuThrAla 91
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68
85
117
115
115
 55
69
86 1
41 1
117 1
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                                                                                                          Best Local Similarity:
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01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                           61.80
55.88%
38.24%
40.66%
                                           PRELIMINARY;
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Query Match:
DB:
                                                                                                                       ORFNames=CG10353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=CG10353;
                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                             Patel S., Phy
Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG10353-PA.
                                                                                                           RE04357p.
                                          Q8MT62
Q8MT62;
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                 RESULT 13
Q8MT62
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                                                                                                                                                                                                               61 TyrLysGlyArgCys--TyrHisileGluProVal------ProGlyGluGluGly- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=15077118; DOI=10.1038/nbt959; Haidelberg J. F., Seahadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Melson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Dimitrov G., Hance M., Tran Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Nat. Biotechnol. 22:554-559(2004).";
                                                                                                                                                                                                   7 TATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 TACCCTGACTCGCCCGGCCTTGGAAGGACGGCTGTATGTGGTATCAGAGTCACCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio. VCBI_TaxID=882;
                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sigma factors serine-protein kinase.
OrderedLocusNames=DVUM0124,
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                         229C3E9FFCE4420B CRC64;
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113
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12
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Oxidoreductase; Photorespiration; Photosynthesis.

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NON TER 436 436
                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                     138 AA
                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                        NOLAN463-2A.SEQ (1-84) x Q6TL49 (1-436)
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                                                                                                                                                                                                                                                       67 ATTAGCAGCTGGTTAGCC 84
                                                                                                                                                                                                                                                                                77 ----GlnTrpileAla 80
                                         48417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 AA; 15178 MW;
                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
62.00
41.38%
41.38%
                                                                                          62.20
39.47$
34.21$
42.03$
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||| :
67 eAspAsp 69
                                         436 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
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                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pDV
                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
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                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                            8303)
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                                                                                                                                                                                                                                                                                                          RESULT 12
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ઠે 요 ð

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685 GluMetLeuileProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 703
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley; Stapleton P., Hong L., Agbayani A., Carlson J., Chample M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., Goorge R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hakapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY118358; AAM4838Y. 1; -. Flybase; Flybase; PRR003349; CG10353. InterPro; IPR007632; DUFS90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 984 AA; 112356 MW; 233EFCAAAD0405E8 CRC64;
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113
112
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                                                                                                     Last sequence update)
Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
984 AA
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                                                                    Created)
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Garg N.S., Gelbart W.M., Glasser K., RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Reinert K., Ramington K., Saunders R.D., Scheeler F., Shen H., Ra Syirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Walliams S.M., Woodager, Worley K.C., Wu D., Yang S., Pan S., Palla S., Sun S., Store R., Wang Z.Y., Massamman D.A., Weinsenbach J., Walliams S.M., Woodager, Worley K.C., Wu D., Yang S., Pan S., Palla S., Pan S., Pan S., Palla S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21426065; PubMed=12537568;
MEDLINE=21426065; PubMed=12537568;
MEDLINE=21426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patel S.D., Peiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a Whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systematic review.";
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FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

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REDUINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., George R.A., Lewis S.E., E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Staten G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Bardon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D., Annil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Baan A., Baxendale J., Bayraktarogul L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolchakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Douck J., Brokstein P., Brottier P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Durbon K., Doug D.E., Downes M., Dugan-Rocha S., Plackenman W., Roden C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Adodek A., Gong F., Gorrell J.H., Harnandez J.R., Harris M., Harvey D., Heinan T.J., Harnandez J.R., Haris M., Harvey D., Heinan T.J., Mernandez J.R., Haris M., Aduston K.A., Howland T.J., Wei M.H., Ibegwam C., Liang Y., Lin X., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLed M.P., Moshrefi A., Moshrefi A., Mong M., Murphy B., Murphy D., Murphy D., Mortherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nelson D.R., Nelson D.R., Nelson R.A., Shen H., Shine B.C., Siden-Klamer R., Saunders R.D., Scheeler F., Shen H., Shine B.C., Siden-Klamer R., Shen H., Shine B.C., Turner R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                744 GluMetLeuileProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 762
                                                                                                                                                                                                                                                                                                                                                         77 CAGCTGCTAATACCCTGACTCGCCCGGCCTTGGAAGGAC-------GGGCTG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                         OEAGBDC5C219FF35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         32 TATGTGGTATCAGAGTCACCAGGATAGA 5
                                                                                                                                                                                                                                                                          Gaps:
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                                                                                                         1043 AA; 118845 MW;
EMBL; AE003487; AAF48110.2; -.
IntAct; Q9YVS8; -.
FlyBase, FBgn0030349; CG10353.
InterPro; IPR007622; DUF590.
Pfam; PF04547; DUF590; 1.
                                                                                                                                                                                        61.80
55.88%
38.24%
40.66%
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                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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                                                                                                         SEQUENCE
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Q76NS2
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77 CAGCTGCTAATACCCTGACTCGCCCGGCCTTGGAAGGAC--------GGGCTG 33
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Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WoodagaT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yehns S.M., WoodagaT, Worley K.C., Wu D., Yang S., Zhong D., Zheng L., Zhorg K.H., Zhorg F.N., Zhong W., Zhou K., Zho S., Zhu K., Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The transposable elements of the Drosophila melanogaster euchromatin
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676365606C1CA98A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TrpTyrLysSerHisGlnAspGln 786
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                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003487; AAN09305.2; -.
Interpro; IPR007632; DUF990.
Pfam; PF04547; DUF90; D
SEQUENCE 1059 AA; 120767 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.80
55.88%
38.24%
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hepatotropic, Fab; hypervariable region, E2 antigen, antibody.
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ID ABG76561 standard; protein; 123
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  WPI; 2002-608502/65.
  WO200260954-A1.
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-MODBLeframe+ n2p.model -DEV=xlp
-Q-/cgn2_1/USPTO 5 spool_DNOLAN08728463-2/runat_04082005_123941_22574/app_query.fasta_1.5
-Q-/cgn2_1/USPTO 5 spool_DNOLAN08728463-2/runat_04082005_123941_22574/app_query.fasta_1.5
-Q-/cgn2_1/USPTO 5 spool_DNOLAN08728463-2/runat_04082005_123941_22574/app_query.fasta_1.5
-DES-MODELS -GFMT-fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pet -THR MAX=LAND 0 -TR MINIS 0 -ALLON=15 -MODE=LOCAL
-OUTPWT-ptc -NORM=ext -HEAPSIZE=500 -MINIER=0 -MAXLENS=2000000000
-USER=NOLAN08728463-2 @CGN 1_1 308 @runat 04082005_123943_22574 -NCPU=6
-LOPU=3 -NO WABP -LARGEQUERY -NES SCORES=0 -WAIT -GSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -YGAPEXT=0.1 -YGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
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148
1 CGGCGAGTCAGGGTATTAG......ACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4211384
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                 protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2105692 seqs, 386760381 residues
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) El antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV El or E2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences AGG76513-ABG76568 represent human monoclonal antibodies against HCV El antigen
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Sequence 123 AA

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25 ArgAlaSerGlyTyrSerPheSerLeuPheTrpValAlaTrpValArgGlnMetProGly 44
                                                                                                                                                                           |||||||::--GluTrpMetAlallelleTyrProGlyAspSerAspThrThrTyrSer 63
                                                                                                                                                                 CAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCACATACAGC
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ADR46829 standard; protein; 411 AA (first entry) 18-NOV-2004 ADR46829; ADR46829 RESULT g ठ

Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.

molecular conjugate; monoclonal antibody; human antigen presenting cell; artigen presenting cell; APC; human; beta human chorionic gonadotropin; betahGG; beta chorionic gonadotropin; antibody; Cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HTV; hepatotropic; virucide; antimalarial; CBB agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HTV; hepatitis; malaria; herpes; antibody B11; pB11-betahCG molecular conjugate; fusion protein. 30-JAN-2004; 2004WO-US002725. WO2004074432-A2. sapiens. 02-SEP-2004 Synthetic. Homo 

Ramakrishna V; 31-JAN-2003; 2003US-0443979P 'n, He WPI; 2004-635555/61. N-PSDB; ADR46828. Keler T, Endres M, (MEDA-) MEDAREX INC

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a

comprises a heavy and/or light chain articlaspen presenting cells (APCBS) inheed to beta human chorionic gonadotropian (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human (YB5-51 or VK-LIS germline sequence with the 98 or 95 amino acid sequences (TB5-51 or VK-LIS germline sequence with the 98 or 95 amino acid sequences (CC CBEQ ID NO:30 or 32 (ABCR4684), respectively, Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single comprises the 411 amino acid sequence of SEQ ID NO:12 (ADCR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjained betahCG, comprising or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCE such that the antigen is processed and carrier, or comprising administering any of the molecular conjugates comprising administering any of the molecular conjugates or presented to T cells in a manner which induces or enhances a T cell-mediated above with APCE such that the molecular conjugates described above, comprising any of the molecular conjugates described above, with APCE such that the antigen. (6) immunostimulatory agent; and (6) inducinally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and conjugate of the antigen and a monoclonal antibody which binds to APCE, and contacting the conjugate either in vivo or exvivo with APCE such that the antigen if membraces a cytotoxic T cell response against the antigen. The molecular conjugate has cytotoxic tricke and antimalarial activities and conjugate of the antigen and a monoclonal antibody which binds to APCE, and confuce and conjugate of and in particular conjugate of the antigen and eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, heparlitis, malaria and herpes. The present sequence represents a human pBl1-betahCG molecular conjugate, which is used in the exemplification of the present invention. present invention describes a molecular conjugate comprising a ocional antibody that binds to human antigen presenting cells (APCs) cytotoxic T cell response in cancers and infectious diseases Claim 16; SEQ ID NO 12; 82pp; English Sequence 411 AA; 

411 26 0 2 137 Length:
Matches:
Conservative:
Mismatches: Indels: 0.000163 113.30 15.76% 15.76% 76.55% Similarity: Percent Similarity: Best Local Similari Query Match: Best

NOLAN463-2B.SEQ (1-84) x ADR46829 (1-411)

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142	123 ValGluIleLvsGlvGlvGlvGlvSerGlvGlvGlvSerGlvGlvGlvGlvGlvSerGlu 142	123
33		33
122	103 AlaThrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122	103
33		33
102	83 GlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnProGluAspPhe 102	83
33		33
82	63 ProLysSerLeulleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer	63
33		33
62		43
33	CGGCCGAGTCAGGGTATTAGCAGCTGGTTAGCC	-

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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determine the presence or level of adipocytes in a cell of tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for fulfiferent types of fat deposits and also be produced e.g. intraabdominal fat associated with heart disease
                                                                                                                                                           183 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyrSer 202
                                   143 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuArgIleSer 162
                                                                                                     163 CysLysGlySerGlyAspSerPheThrThrTyrTrpIleGlyTrpValArgGlnMetPro 182
   33
                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody, adipocyte, heavy chain, light chain, obesity, fat, heart disease, complementarity determining region, CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-adipocyte monoclonal antibody heavy chain, FAT 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 144; 182pp; English.
                                                                                                                                                                                                                                                                                                                   AAU02582 standard; protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2000; 2000WO-GB003900.
                                                                                                                                                                                                                                  99US-0158812P
                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                             70 CCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edwards BM, Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-282031/29.
N-PSDB; AAS03482.
                                                                    33 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200127279-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                          AAU02582;
33
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Alignment Scores:

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their active domains. The polypectides encoting and intentions of their active domains. The polypectides of olymentides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the abbrrant protein care superson or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides or used to identify compounds which bind to the polypeptides.

The polypeptides of the invention are used as probes and primers, for sequencing, for crombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein antibodies at issue markers, and to isolate receptors or ligands.

Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to polynucleotides encoding novel human proteins or
                                                                                                                                                                        61
                                                                                                                                                                                            GGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
122
20
20
3
3
9
Length:
Matches:
Conservative:
Mismatches:
                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 554-555; 894pp; English.
                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue regeneration; immune disorder.
                                                                                                                                 NOLAN463-2B.SEQ (1-84) x AAU02582 (1-122)
                                                                                                                                                                                                                                                62 CATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                      59 rgTyrSerProSerPheGlnGly 66
                                                                                                                                                                                                                                                                                                                                                             AAU14177 standard; protein; 474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001; 2001WO-US002623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2000; 2000US-00491404
 0.000801
                 106.20
66.67%
60.61%
71.76%
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel protein #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451939/48.
                                     Percent Similarity:
Best Local Similarity:
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                                                                               Query Match:
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90
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ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating offeroporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fingal infection or from autoimmunity, cancer, allergy, asthma, graftversus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention
                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                                                                                            Improved method for antibody treatment - uses an antibody comprising an Old World monkey variable region and a human constant domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-CD4 antibody; monkey; human; therapy; variable heavy domain; old World monkey; constant domain; eczema; immuno-modulated disease;
                                                                                                                                                                                                                                                                   --- GGGTATTAGC-
                                                                                                                                                          474
23
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2
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                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                         Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW54008 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00735064.
92US-00856281.
92US-00912292.
95US-00379072.
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47.17%
43.40%
70.54%
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis.
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                                                                                                                                                                                                                                                                   GGCGAGTCA-
                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                         Sequence 474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                               Alignment Scores:
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10-JUL-1992;
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29-JUL-1998
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This sequence is the consensus VH5 domain of an anti-CD4 antibody (Ab). This sequence can be used in the method of the invention for treating a mubject, where the treatment comprises administration of an Ab. The method comprises the administration of an antibody which has an Old World monkey (e.g. baboon or macaque) variable region which binds to an antigen (Ag) (or Ag binding portion), and a human constant domain. The method is useful for the treatment of ecreme and immuno-modulated diseases and especially rheumatoid arthritis. The recombinant antibodies used are sufficiently different from native monkey antibodies to allow human antibodies used in therapy in prior art, these antibodies do not induce human anti-antibodies used in therapy in prior art, these antibodies do not induce human anti-antibodies on repeated administration. They also have longer half-lives and do not have a lack of effector function with human cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGluSerLeuLys1leSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGly1le1leTyrProGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Fv molecule hypervariable region related peptide #108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Szanton
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PR field.)
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103.40
45.28%
43.40%
69.86%
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, Peretz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-619166/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Fv
disulfide
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Query Match:
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No.:
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characteristics so as to selectively bind target cell in favor of other Claim 13; Page 205; 232pp; English. 

The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is chain Fv (acFv) or a disulfide Fv (aFv). The peptide, optionally in sesociation with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, as accoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region created peptide of the invention

Sequence 98 AA;

Matches: Conservative: Mismatches: Indels: Length: 0.00163 103.40 45.28% 43.40% 69.86% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

NOLAN463-2B.SEQ (1-84) x ABG78233 (1-98)

21 47 54 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34 ----AGCTGGTTAGCCATCATCTATCCTGG 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 3 GGCGAGTCA-----GGGTATTAGC 84 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 48 22 g 셤 셤 È õ ò

RESULT 7

ABG78231 standard; protein; 98 AA ABG78231;

(first entry) 15-NOV-2002 Human Fv molecule hypervariable region related peptide #106.

Human; Fv molecule, hypervariable region, single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

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WO200259264-A2.

01-AUG-2002

31-DEC-2001; 2001WO-US049440. 29-DEC-2000; 2000US-00751181

(BIOT-) BIO-TECHNOLOGY GEN CORP.

Levanon A; Szanton E, Guy R, Lipschitz O, Hagai Y, Lazarovits J, Plaksin D, Peretz T; 

The invention relates to a peptide or polypeptide comprising an Fy molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, bastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other Claim 13; Page 204; 232pp; English WPI; 2002-619166/66. 

ä Sequence 98

GlyGluSerLeuLys1leSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrp11 ---GGGTATTAGC-28 1 28 Length: Matches: Conservative: Mismatches: Indels: NOLAN463-2B.SEQ (1-84) x ABG78231 (1-98) 0.00163 103.40 45.28% 43.40% 69.86% Percent Similarity: Best Local Similarity: Alignment Scores: 15 Query Match: Score: 8 셤

-----AGCTGGTTAGCCATCATCTATCCTGG -----22

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TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84

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48

34 47 54

> RESULT 8 ABG78232

ABG78232 standard; protein; 98

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ABG78232;

15-NOV-2002 (first entry)

Human Fv molecule hypervariable region related peptide #107.

Human; Fv molecule, hypervariable region, single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia. 

Homo sapiens

WO200259264-A2

01-AUG-2002.

31-DEC-2001; 2001WO-US049440.

29-DEC-2000; 2000US-00751181

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                                                                                                                                             Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
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                                                       Levanon A;
                                                       Guy R, Lipschitz O, Szanton E,
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Matches:
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                                                                                                                                                                                                                                          Claim 13; Page 204-205; 232pp; English.
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                   (BIOT-) BIO-TECHNOLOGY GEN CORP
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                                                       Lazarovits J,
                                                                          Peretz T;
                                                                                                            WPI; 2002-619166/66.
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Best Local Similarity:
Query Match:
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                                                   Hagai Y, La
Plaksin D,
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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one artibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases, inflammatory diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases cantionadus diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases caused by sulphated tyrosine-dependent protein-cells in interactions. This sequence represents a human antibody fragment
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                                                                                                                                                                                                                                                                                                                                                           Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
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Levanon I
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Peretz T,
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Matches:
Conservative:
Mismatches:
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Kooperman L,
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Amit B, K
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                                                                                                                                                                                (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                  31-DEC-2001; 2001WO-US049442.
                                                                                                     29-DEC-2000; 2000US-00751181
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Richter T,
                                                                                                                                                                                                                                                                                                           WPI; 2002-674776/72.
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Query Match:
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Szanthon E,
11-JUL-2002
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ID ABG9
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GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complete being bound by an antibody, its antigen-binding fragment or its complete being bound by an antibody, its antigen-binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, for increasing mortality of tumour or leukaemia dents. The disease cells for increasing the susceptibility of diseased cells to decreasing the number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to for decreasing the number of tumour or leukaemia cells, for increasing the anticance or anticoned purposes. The epitopes are useful for diseases, inflammatory diseases such as cancer, leukaemia, autoimmune diseases, inflammatory cells singular diseases such as mentically infarction, cretinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-

of the interactions. This sequence represents a human antibody fragment
                                                                                                                       Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Amit B, Kooperman L, Peretz T, Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated epitope present on cancer cells and important in physiclogical phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
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Matches:
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                                                                                Human antibody fragment #106.
                                                                                                                                                                                                                                                                                                                                                                            31-DEC-2001; 2001WO-US049442.
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                                       04-DEC-2002 (first entry)
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, Richter T,
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Szanthon E,
                                                                                                                                                                                                                                                                                                                                11-JUL-2002.
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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one attibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune cepitopes are useful for inhibiting cell rolling, inflammation, autoimmune tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anticortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to decreasing the number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases, inflammatory diseases such as myocardial infarction, cretinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-
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                                                                                                                                                                                                                                                                                                                   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                      Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
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Levanon A;
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Peretz T,
                                                                       84
                                                                                          Plaksin D, Vogel T, Amit B, Kooperman L,
                                                                     TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
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                                                                                                                                                                                                                                                                                    Human antibody fragment #107.
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29-DEC-2000; 2000US-0258948P.
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Richter T,
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Conservative: Mismatches: Indels:

103.40 45.28% 43.40% 69.86%

Similarity:

Percent Similarity: Best Local Similari

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Query Match:

Gaps:

NOLAN463-2B.SEQ (1-84) x ABG91922 (1-98)

3 GGCGAGTCA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour; cancer; systemic lupus erythematosus; immunoglobulin constant region; immunoglobulin variable region; autoimmune response; rheumatoid arthritis; eczema; lymphoma; immunomodulatory disease; leukaemia; Hashimoto's thyroiditis; autoimmune carditis; Addison's disease; type I-diabetes mellitus; multiple sclerosis; male infertility; autoimmune hemolytic anaemia; inflammatory bowel disease; Sjogren's syndrome; psoriasis.
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92US-00856281.
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95US-00476237.
98US-00082472.
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   Sequence 98 AA;
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07-JUN-1995;
21-MAY-1998;
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23-MAR-1992;
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immunoglobulin variable region. The first and second Old World monkey can be the same or different. The recombinant antibody is useful for treating a human having the antigen described above, e.g. for treating cancer in a human having a tumour antigen, or for treating a human suffering from an autoimmune response (where the antigen is involved in an autoimmune response in the human). In particular, the recombinant antibody is useful for treating rheumatoid arthritis, eczema, or an immunomodulatory disease. The recombinant antibody is also useful for treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis, autoimmune carditis, Addison's disease, type I-diabetes mellitus, multiple sclerosis, male infertility, autoimmune hemolytic ansemia, inflammarory bowel disease, Sjogren's syndrome, psoriasis, or systemic lupus erythematosus. This is sloslypeptide for creation of the recombinant antibody
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GlyGluSerLeu***11eSerCy8Ly8Gly8erGlyTyr-SerPheThrSerTyrTrpIl
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Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures into

structural ensembles.

WPI; 2003-093043/08

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The present invention describes a method for identifying and obtaining an inhibitor of a pathological process. The method comprises determining if a compound is capable of modulating the binding of the Rc-epsilon-R1 receptor alpha-chain and an autoantibody against the Rc-epsilon-R1 receptor alpha-chain for identifying and obtaining an inhibitor of a pathological process; (2) use of the identified inhibitor for inhibiting activity of the autoantibody against the Rc-epsilon-R1 receptor alpha-chain, and (3) a compound identified by the method, which binds but does not activate the autoantibody against the Rc-epsilon-R1 receptor alpha-chain. The method is useful for obtaining an inhibitor of a pathological process e.g. imbalance between cell-bound and free IgE e.g. allergic disease (urticaria, late phase allergic reactions, intrinsic asthma, drug intolerance and food intolerance). IgE mediated disease or malignancy. The compound is useful for treating a pathological process, particularly conditional autoimmunity. The present sequence have been an abana recombinant anti-Fc-epsilon-R1 alpha autoantibody beautoantibody against the presents and the present sequence.
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 modulating the binding of the Fc-epsilon-R1 receptor and an
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                                                                                                                                                                                                                                                                                                                                                                   heavy chain protein sequence from the present invention
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                  autoantibody against its alpha-chain.
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                                                Page 22; 29pp; English.
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17-APR-2002; 2002WO-US012202 17-APR-2001; 2001US-0284407P

24-OCT-2002

(ABMA-) ABMAXIS INC

The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, poppides and nucleic acids. The libraries constructed are useful as a Source of antibody candidates for further screening for novel antibodies with high affainty against a wide range of antigens and having no or minimum immunogenecity to human subjects treated with antibody therapeutics. This sequence repersents a human peptide region of an antibody relating to the novel antibody library construction method of 21 54 47 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl -----AGCTGGTTAGCCATCTATCTTGG Human germline heavy chain variable region gene segment #45. Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type. 84 Length:
Matches:
Conservative:
Mismatches: TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC Indels: Disclosure; Page 109-110; 119pp; English NOLAN463-2B.SEQ (1-84) x ABJ18687 (1-98) ABO27112 standard; protein; 98 AA 0.00163 103.40 45.28% 43.40% 69.86% 3 GGCGAGTCA------(first entry) Percent Similarity: Best Local Similarity: Query Match: DB: US2003039649-A1 Sequence 98 AA; 10-SEP-2003 Homo sapiens 27-FEB-2003 ABO27112; 54 48 22 RESULT 15 AB027112 #X#X#####X#X#OOOOOOOOOOOO 엄 ઠે 셤 ò 요 ઠે

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comprising making chimeric antibodies containing a complementarity determining making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a for selection, for humanised antibody of sequence of any subject species to a less immunogenic form suitable for use in an object species to a less immunogenic form suitable for use in an object species to a less converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species that retain con-human CDR regions and to provide humanisch antibodies that retain this antitable human for sequences to support of for direct comparison of framework sequences, without the need for determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing framework sequences between non-human antibodies. This sequence represents a human heavy chain variable region gene segment used in the creation of humanised antibodies
                                                                                                                                                                                                                                                              Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of making a humanised antibody
                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 31pp; English
12-JUL-2002; 2002US-00194975.
                                                  12-JUL-2001; 2001US-0305111P.
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34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54 ---GGGTATTAGC------- 21 -------AGCTGGTTAGCCATCATCTATCCTGG 26 26 26 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: NOLAN463-2B.SEQ (1-84) x ABO27112 (1-98) 3 GGCGAGTCA------103.40 45.28% 43.40% 69.86% 0.00163 Percent Similarity: Best Local Similarity: Query Match: 22 -----Alignment Scores: Pred. No.: 48 셤 유 ò ઠે ð

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Search completed: August 4, 2005, 18:55:57 Job time: 93 secs

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Sequence 48,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 23-JAN-1992
PRIOR APPLICATION DATA:
               US-09-490-153-40
US-09-490-153-40
US-09-490-153-67
US-09-490-134-67
US-09-490-324-67
US-09-165-219A-171
US-08-665-202-44
US-09-315-574-44
US-09-315-574-5
US-09-956-086-4
US-09-956-086-4
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US-09-956-087-4
US-09-915-574-6
US-08-665-202-55
US-09-315-574-48
US-09-315-574-56
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 4, 2005, 18:44:26; Search time 22.25 Seconds (without alignments) 563.642 Million cell updates/sec
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1 CGGCGAGTCAGGGTATTAG.....ACAGCCCGTCCTTCCAAGGC
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6: /cgn2_6/ptodatcal/iaa/PcTUS_COMB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                        OM nucleic - protein search, using frame_plus_n2p model
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US-08-476-349A-81
US-08-665-202-33
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US-09-490-123-26
US-09-490-133-26
US-09-025-769B-40
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Listing first 45 summaries
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Sequence 1.75-0105

Settle No. 5750105

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA.
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APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY, AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY SYTEM:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.000271
103.40
45.28%
43.40%
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Best Local Similarity:
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Pred. No.:
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US-08-65-202-33
US-08-65-202-32
US-08-65-202-3
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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTONNEY, ACENT INFORMATION:
NAME: Teskin E8q., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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COMPUTER: IBM Compatible
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
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Query Match:
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US-08-545-809A-133
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                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Batent No. 6512097

GENERAL INFORMATION:

APPLICANT: Marke, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.

STREET: FOUL EMbarcadero Center, Suite 1100
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TRAPPE Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NDATA:
APPLICATION NUMBER: 20.042-99
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                      NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
          APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIPRICATION: 424
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
ATTORNEY/AGENT INFORMATION:
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45.28%
43.40%
69.86%
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 -----
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                  TYPE: amino STRANDEDNESS:
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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: BEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
NUMBER OF SEQUENCES: 145
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 .----AGCTGGTTAGCCATCATC
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Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PULICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UNN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66,202
FILING DATE: 13-UNN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HURLEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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Query Match:
DB:
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ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PACTEULIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698

TITING DATE: 18-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: James F. Haley, Jr., Egq. c/o Fish & Neave 1251 Avenue of the Americas
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APPLICANT: Knappik, Peter
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
WINMER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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Mismatches:
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Matches:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGIGTRATION NUMBER: 29,066
REGIGTRATION NUMBER: 06501/004001
TELEPHONE: 617-542-5070
TELEFACOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-806
TELEFAX: 617-542-806
TELEFAX: 617-542-806
TELEFAX: 617-812-806
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-025-769B-26; Sequence 26, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
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45.28%
43.40%
69.86%
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MOLECULE TYPE: protein

US-08-545-809A-133
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STATE: New York
COUNTRY: USA
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Best Local Similarity:
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STREET: 12
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Pred. No.:
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DB:
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34 eGlyfrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlylleileTyrProGl 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------AGCTGGTTAGCCATCATCTATCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ge, Liming
Moroney, Simon
Plueckthuu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      119
23
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26
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09490070A, Patent No. 6696248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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COMPUTER READABLE FORM:
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103.40
45.28%
43.40%
69.86%
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                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 -----
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Best Local Similarity:
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ZIP: 10021
COMPUTER READABLE FORM:
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45.28%
43.40%
69.86%
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION
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Best Local Similarity:
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US-09-490-324-26
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNIA...
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.30 (EP/
TOFTWARE: PatentIn Release #1.30 (EP/
TOFTWARE: PatentIn Release #1.3
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Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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23
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/490,153 FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26
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Patent No. 6706484
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION
                                                                                         INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acidd
TYPE: amino acid
                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              0.00029
103.40
45.28%
43.40%
69.86%
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                                                            TELEFAX: (202)
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Best Local Similarity:
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Pred. No.:
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15 GlyGluSerLeuLyg1leSerCygLygGlySerGlyTyr-SerPheThrSerTyrTrp11 34
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Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                          119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         NOLAN463-2B.SEQ (1-84) x US-09-490-153-26 (1-119)
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REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09490324
Patent No. 6928422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
TYPE: amino acid
                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
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Pack, Peter
Ilag, Vic
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Sequence 67, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
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TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                      0.00029
                                                                                                                                                                       103.40
45.28%
43.40%
69.86%
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                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                      Alignment Scores:
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APPLICANT: Rack, Peter
APPLICANT: 11ag, Vic
APPLICANT: 1.0 (1.0 (1.0 c.))
APPLICANT: 1.0 (1.0 c.)
APPLICANT: PluckThun, Andreas
APPLICANT: PluckThun, Andreas
APPLICANT: PluckThun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DatentIn Release #1.0, Version #1.30 (EPO)

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

PRIJNG DATE: 18-FEB-1998

PRIJNG DATE: 18-FEB-1998

APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., ESq.

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794
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23
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26
                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
       TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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45.28%
43.40%
69.86%
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Best Local Similarity:
Query Match:
DB:
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CITY: New York
STATE: New York
COUNTRY: USA
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Pred. No.:
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34 eGlyfrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlylleIleTyrProGl 54
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                                                                                                                                                                                                                                                                                                     -------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
WUMBER OP SEQUENCES: 373
CORRESPONDENCE ADDRESS:
  120
23
1
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26
2
                                                                                                                                                                                                                                                                                                                                                                                                                           48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James P. Haley, Jr., Esq.
REGISTAATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                        Gaps:
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TOPOLOGY: Inhear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-490-070A-67
                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
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SEQUENCE CHARACTERSISICS:
LENGTH: 120 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                              103.40
45.28%
43.40%
69.86%
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                  22 -----
                                             Percent Similarity:
Best Local Similarity:
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   Alignment Scores:
Pred. No.:
                                                                       Query Match:
DB:
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15 GlyGluSerLeuLyBIleSerCyBLyBGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
                                                                                                                                                                                                                                               -----AGCTGGTTAGCCATCTTCTTGG 47
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                                                                                                                                                                                                                                                               34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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                                             120
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                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELEPHONE: (202) 912-2000
TELEPHONE: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 120 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
                                                          103.40
45.28%
43.40%
69.86%
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                   3 GGCGAGTCA
                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
US-09-025-769B-67
                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                      48 IGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                              NOLAN463-2B.SEQ (1-84) x US-09-490-070A-40 (1-120)
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Matches:
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Pred. No.:
Score:
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TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                            US-09-490-153-67; Sequence 67, Application US/09490153

Patent No. 6706484

GENERAL INFORMATION:
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LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 67
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103.40
45.28%
43.40%
69.86%
43.40%
69.86%
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                     Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                            ----GGGTATTAGC---
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 Conservative:
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APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                Mismatches:
Indels:
Gaps:
                                                                           NOLAN463-2B.SEQ (1-84) x US-09-490-070A-67 (1-120)
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Matches:
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MCDIUMTYER: THOPPY COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                               RESULT 14
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 40
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                         Pack, Peter
Ilag, Vic
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                 Best Local Similarity:
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Score:
Percent Similarity:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
Mismatches:
Indels:
Gaps:
                                                                          NOLAN463-2B.SEQ (1-84) x US-09-490-153-40 (1-120)
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67
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Run on:

Sequence:

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Jequence 85,
Sequence 45, App.
Transe 16, Appl.
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(Sequence 49, Application US/10466242

(Sequence 49, Application US/10466242

(Sequence 49, Application No. US2004020887A1

(GENERAL INFORMATION:

(APPLICANT: Dersenberg, Katarina

(APPLICANT: Persen), Mate

(TILE REFERENCE: 0380-P03249US00

(CURRENT APPLICATION NUMBER: US/10/466,242

(CURRENT PILING DATE: 2004-01-16

(PRIOR APPLICATION NUMBER: PCI/SE02/00044

(NUMBER OF SEQ ID NOS: 56

(SOFTWARE PATENTIN VERSION 3.1

(SEQ ID NO 49)
                                                                                                              Sequence 49, App
                                                                                                                                                               Sequence 284,
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Sequence
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US-10-125-687-16
US-10-041-860-301
US-10-041-860-312
US-10-041-860-312
US-10-041-860-312
US-10-041-860-313
US-10-041-860-313
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US-10-041-860-313
US-10-041-860-314
US-10-041-860-316
US-10-041-860-316
US-10-041-860-316
US-10-041-860-316
US-10-032-988B-106
US-10-032-98BB-107
US-10-032-98BB-108
US-10-032-926B-106
US-10-032-926B-107
US-10-032-927-107
US-10-032-927-90
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ORGANISM: Homo sapiens
                          Query
Match
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                             Result
No.
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-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                            4, 2005, 19:01:38; Search time 78.75 Seconds (without alignments) 832.849 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                           CGGGCGAGTCAGGGTATTAG.....ACAGCCCGTCCTTCCAAGGC
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/DFMW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
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22: /cgn2_6/ptodata/1/pubpaa/US10B_W PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                   - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1752860 seqs, 390397842 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 2000000000
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Database :

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Sequence 284, Application US/10291265

Sequence 284, Application US/10291265

Publication No. US20030222054A1

GENERAL INFORMATION:

APPLICANT: Hyaeq, Inc.

APPLICANT: Tang et al.

ITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-017

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/617,746

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR PILING DATE: 2000-07-17

PRIOR PLILNG DATE: 2000-08-03

PRIOR PLILNG DATE: 2000-08-03
                                                                                                                              123 ValGluIleLysGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlyGlyGlySerGlu 142
                                      103 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122
                                                                                                                                                                                                                       143 ValGlnLeuValGlnSerGlyAlaGluValLysPysProGlyGluSerLeuArglleSer 162
                                                                                                                                                                                                                                                                                                               163 CysLysGlySerGlyAspSerPheThrTyrTrpIleGlyTrpValArgGlnMetPro 182
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Matches:
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US-10-291-265-284
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Best Local Similarity:
Query Match:
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US-10-769-144-12

i Sequence 12, Application US/10769144

j Publication No. US20040248215A1

j GENERAL INFORMATION:
    APPLICANT: Realer, Tibor

j APPLICANT: Endres, Michael

APPLICANT: Remarkrishna, Venky

TITLE OF INVENTION: THEREOR

j TITLE OF INVENTION: ANTIBER: 05/443979

k FILOR APPLICATION NUMBER: 60/443979

k RIOR APPLICATION NUMBER: 60/443979

j RIOR FILING DATE: 2003-01-31

j NUMBER OF SEQ ID NOS: 32

j SOFTWARE: FASTSEQ for Windows Version 4.0

j SEQ ID NO 12

j TYPE: PRT

j ORGANISM: Homo sapiens
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Matches:
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                   COCATION: (1)..(123)
CIHER INFORMATION: Clone 2b:7 VH
US-10-466-242-49
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Best Local Similarity:
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  NAME/KEY: PEPTIDE
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ORGANISM: Homo sapiens
FEATURE:
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US-10-194-975-45
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US-10-125-687-16
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Sequence 89. Application US/09850165

Settent No. US20020150580A1

GENERAL INFORMATION:

APPLICANT: NEWMAN, ROLAND A.

APPLICANT: HANNA, NABIL

APPLICANT: RAAB, RONALD W.

TILE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY

TILE REFERENCE: 037003-0280614

CURRENT APPLICATION NUMBER: US/09/850,165

CURRENT FILING DATE: 2001-05-08

PRIOR FILING DATE: 1998-05-21

PRIOR PLING DATE: 1998-05-21

PRIOR PLING DATE: 1995-04-17

PRIOR PLING DATE: 1995-04-17

PRIOR PLING DATE: 1992-07-10

PRIOR PLING DATE: 1992-07-25

NUMBER OF SEQ ID NOS: 114

SEOFWARE: PALEGATION VUMBER: 07/735,064
                                               Sequence 114, Application US/10002631C
Publication No. US20030157486A1
GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REPERENCE: A34943 090495.0243
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                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (2)...(66)
OTHER INFORMATION: Xaa = any amino acid
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66.67%
57.58%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 301
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LENGTH: 98
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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Publication No. US20030039649A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Super Humanized Antibodies
TITLE OF INVENTION: Super Humanized Antibodies
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT PILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR APPLICATION NUMBER: US 60/305,111
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 98
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Matches:
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NAME/KEY: MOD RES
LOCATION: (19)
COTHER INFORMATION: Arg or Lys
US-09-850-165-89
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103.40
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Best Local Similarity:
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45.28%
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ORGANISM: homo sapiens
US-10-041-860-301
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Best Local Similarity:
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Sequence 16, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SSPUARE: Patentin version 3.1
ENGTH: 98
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| Sequence 6, Application No. US20030157109A1
| GENERAL INPORMATION:
| APPLICANT: Corralm, Jose R.F. |
| APPLICANT: Feng, Xiao-Chi |
| APPLICANT: Feng, Xiao-Chi |
| APPLICANT: Tang, Xiao-Chi |
| APPLICANT: Tang, Xiao-Chi |
| APPLICANT: Chen, Francine |
| APPLICANT: Chen, Francine |
| APPLICANT: Chen, Francine |
| APPLICANT: Meber, Richard |
| APPLICANT: Bezabeh, Binyam |
| TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES |
| TITLE OF INVENTION: THEREOF |
| FILE REFERENCE: ABGENIX.051A |
| CURRENT FILING DATE: 2002-01-07 |
| NUMBER OF SEQ ID NOS: 377 |
| SOCTHARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 6 |
| LENGTH: 98 |
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ORGANISM: homo sapiens
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ORGANISM: Homo sapiens
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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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US-10-041-860-301

Sequence 301, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Chen, Francine

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Gazit, Gadi

APPLICANT: Heng, Xiao-Dng

APPLICANT: Tang, Xiao-Dng

APPLICANT: Arg, Xiao-Dng

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ATTIBODIES DIRECTED TO PDGFD AND USES

TITLE OF INVENTION: ATTIBODIES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTI
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APPLICANT: Corvalan, Jose R.F.; APPLICANT: Feng, Xiao-Chi; APPLICANT: Yang, Xiao-Dong; APPLICANT: Chen, Francine; APPLICANT: Weber, Richard; APPLICANT: Weber, Richard
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APPLICANT: Bezabe	sh, Binyam				rcent Similari	ţ
; IIILE OF INVENTION: ANIBODIES DIRECTED TO FUGED AND USES; TITLE OF INVENTION: THEREOF; FILE REFERENCE: ABGRENIX.051A	HEREOF  SGENIX.051A	IKECIED IO PDGF	D AND USES	DBes Oue	Best Local Similar: Query Match: DR:	ar
; CURRENT APPLICATION NUMBER: US/10/041,860; CURRENT FILING DATE: 2002-01-07 . MITMAED OF SEC IT MOS. 377	ON NUMBER: US/10 TE: 2002-01-07	)/041,860		N N	NOLAN463-2B.SEQ	ij
SOFTWARE: FastSEQ for Windows Version	for Windows Ver	rsion 4.0		<i>&amp;</i>	3 960	Ö.
; SEC ID NO 302 ; LENGTH: 98 · TYDE: DDT				<b>q</b> a	   	=ંદ્ર
; ORGANISM: homo sapiens ; PRATIDE:	ıpiens			8	22	į
; NAME/KEY: VARIANT				- A	34 eGly	7
O	1: Xaa = Any Amino Acid	ino Acid		۲۵ 	48 TGAC	AC.
; NAME/KEY: VARIANT ; LOCATION: 23				අ <sub>ධ</sub>	1    54 yAsp6	_ g
; OTHER INFORMATION: Xaa US-10-041-860-302	I: Xaa = Any Amino Acid	ino Acid		RE	RESULT 12 US-10-041-860-318	ω,
Alignment Scores: Pred. No.: Score:	0.00316 103.40	Length: Matches:	98 23		Sequence 318, App Publication No. 1 GENERAL INFORMATJ APPLICANT: Corve	A T
Percent Similarity: Best Local Similarity Query Match:	45.28% 43.40% 69.86%	Conservative: Mismatches: Indels:	e: 1 3 26	. 16 16 16		Jia, Fenc Yang
NOLAN463-2B.SEQ (1-84)	×	daps: 160-302 (1-98)	4			Gazi
Oy 3 GGCGAGTCA	CA	(555	GGTATTAGC21	** **	APPLICANT: Bezz	Beza
Db 15 GlyGluSe	  erLeuLysIleSerC	  ys***GlySerGly			TITLE OF INVENTI FILE REFERENCE:	Z :: 2
22		AG	AGCTGGTTAGCCATCATCTATCCTGG 47		CURRENT FILING I	35H
Db 34 eGlyTrp	<b>ValArgGlnMetPr</b> c	oglyLysGlyLeuGlı	eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyileilefyrProGl 54		SOFTWARE: FastS	tSE
Oy 48 TGACTCTC	48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84	CCGTCCTTCCAAGG	46 4	-	LENGTH: 98 TYPE: PRT	;
	aspilitatgiyiser	rioser Filedillot)	00	sn ns·	; OKGANISM: DOMO US-10-041-860-318	ရှိ ဆ
RESULT 11 US-10-041-860-312 ; Sequence 312, Application US/10041860 ; Publication No. US20030157109A1	cation US/10041	.860		Alig Pred Scor	Alignment Scores Pred. No.: Score:	
; APPLICANT: Corvalan, Jose ; APPLICANT: Jia, Xiao-Chi	orvalan, Jose R.F. Jia, Xiao-Chi			O B B B	Percent Similarity Best Local Similar Query Match:	ari
	Feng, Xiao Yang, Xiao-Dong			DB:		:
	Cnen, Francine Gazit, Gadi			ION	∞ .	Ė
; APPLICANT: Weber,	weber, Kıchard Bezabeh, Binyam	ŕ		<i></i> ∂	 E	5 5 5 5 5 5 5 7 7 7 7 7
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES ; TITLE OF INVENTION: THEREOF	: ANTIBODIES DI	RECTED TO PDGFI	) AND USES	qq	15 ĠlyĠl	<u>g</u>
; FILE REFERENCE: AB( ; CURRENT APPLICATION	GENIX.051A N NUMBER: US/10	/041,860		Š	22	i
; CURRENT FILING DATE:	E: 2002-01-07		-	qa 	34 eGlyT	17.
		sion 4.0		λο	48 TGACT	5
; LENGTH: 98 ; TYPE: PRT				qá	54 yAspS	30gs
ORGANISM: homo sap US-10-041-860-312	sapiens			REG	RESULT 13 US-10-041-860-320	ام
Alignment Scores: Pred. No.: Score:	0.00316 103.40	Length: Matches:	98 23		sequence 320, App Publication No. U GENERAL INFORMATI APPLICANT: Corva	PTI P
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YTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIlelleTyrProGl 54
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3luSerLeuLys1leSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrp11 34
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Jia, Xiao-Chi
Feng, Xiao-Chi
Feng, Xiao-Dong
Chen, Francine
Gazit, Gadi
Weber, Richard
Bezabeh, Binyam
Weber, Richard
Bezabeh, Binyam
With ANTIBODIES DIRECTED TO PDGFD AND USES
TOWN ANTIBODIES DIRECTED TO POGFD AND USES
TOWN ANTIBODIES DIRECTED TO POGFD AND USES
TEATION NUMBER: US/10/041,860
LICATION NUMBER: US/10/041,860
LING DATE: 2002-01-07
SQ ID NOS: 377
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US20030157109A1
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No. US20030157109A1
DRMATION:
Corvalan, Jose R.F.
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; ORGANISM: homo sapiens
US-10-041-860-336
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US-10-041-860-367
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US-10-041-860-336

is Sequence 336, Application US/10041860

is Publication No. US20030157109A1

is GENERAL INFORMATION:
is APPLICANT: Corvalan, Jose R.F.
is APPLICANT: Vang, Xiao-Chi
is APPLICANT: Yang, Xiao-Chi
is APPLICANT: Weber, Riao-Chi
is APPLICANT: Weber, Richard
is APPLICANT: Head, Xiao-Dong
is APPLICANT: Weber, Richard
is APPLICANT: Weber, Reference Region
is APPLICANT: Weber, Reference Reference Region
is APPLICANT: Weber, Reference Reference Region
is APPLICANT: Weber, Reference Reference Region
is APPLICANT:
                                                                  APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFRENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 320
LENGTH: 98
TVDR: PRI
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LOCATION: 68
OTHER INFORMATION: Xaa = Any Amino Acid
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US-10-041-860-320
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Yang, Xiao-Dong
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  Jia, Xiao-Chi
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ORGANISM: homo sapiens
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Best Local Similarity:
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NAME/KEY: VARIANT
LOCATION: 68
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                                                                      NOLAN463-2B.SEQ (1-84) x US-10-041-860-336 (1-98)
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                  Percent Similarity:
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Search completed: August 4, 2005, 19:30:18 Job time: 79.75 secs

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Sequence:

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Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrosomy A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
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A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;19-102/Domain: immunoglobulin homology <IMM>
     Length:
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-MODEL=frame+ n2p.model -DEV=xlp
-O=/Cggn2_1/USFTO spool p/NOLAN08728463-2/runat_04082005_123844_22592/app_query.fasta_1.5
-O=/Cggn2_1/USFTO spool p/NOLAN08728463-2/runat_04082005_123844_22592/app_query.fasta_1.5
-DB=FIR -QFWT=fastan -SUFFIX=rpr -MINMATCH=0.1-LCOPCL=0.LCODEEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORMe=xt -HEAPSTZE=560 -MINIEN=0 -MAXIEN=200000000
-USFR-NOLAN08728463-2_@CGN -1 7 @runat_04082005_1239422592 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DESPLOCK=100 -LONGUCG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                 OM nucleic - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH1274
B;Cai, J; Humphries, C; Richardson, A; Tucker, P.W.
J; Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human A;Title: Extensive and selective mutation of a rearranged VH5 gene in human A;Reference number: PH1232; MUD:93018822; PMID:1402653
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-98 <CAI>A;Resperimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
Ig heavy chain V region (clone P1-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1409
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High ir
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                                                                                                                   A; Accession: PH1409
A; Molecule type: mRNA
A; Residues: 1-127 < VAN>
A; Residues: 1-127 < VAN>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
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Db 18 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 37	Oy 48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlylleIleTyrProGl	1
48 TGACTCTGATACCACATACAGCCGGTCCTTCCAAGGC 84	PH1266 Ig heavy chain V region (clone VERGS) - human (fragment) C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
RESULT 6 \$12424 B heavy chain V region (5) - human C.Gardies Home caries (man)	C;Accession: FHizbo R;Cartession: Humphries, C.; Richardson, A.; Tucker, P.W. J; Exp. Med. 176, 1073-1081, 1992 A;Title: Extensive and ablective mutation of a rearranged VH5 gene in human B cell chron
Procession: Saprens (Man) coession: S12424; S12425; S12426; S12427; S12429; S12432 anz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.	Afrecence number: FALZ32; MULD:93018822; FMLD:1402653 Afaccession: PH1266 Afroceule type: mRNA Afresidues: 1-102 <cai></cai>
30 J. 8, 3741-3748, 1989 Title: The smaller human V(H) gene families display remarkably little polymorphism. Reference number: \$09421, WUD:90059975, PMID:2511001 Accession: \$12424	A:Experimental source: EBV-transformed CD5+ B cell [from adult PBL] C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;19-102/Domain: immunoglobulin homology <imm></imm>
Status: preliminary; translation not snown Aolecule type: DNA Aesidues: 1-101 <san> Tross-references: EMBL:X56372</san>	Alignment Scores: 0.000145 Length: 102 Pred. No.: Score: 103.40 Matches: 23
Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT Accession: \$12425 Status: translation not shown	Percent Similarity: 45.28% Conservative: 1 Best Local Similarity: 43.40% Mismatches: 3 Query Match: 69.86% Indels: 26
Autoriar type: June Autoriar type: June Toss-references: EMBL:X56373	. caps: AN463-2B.SEQ (1-84) x PH1266 (1-102)
Accession: 512426 Status: translation not shown Aolecule type: DNA Residues: 1-101 <sa3></sa3>	Oy 3 GGCGAGTCA21 
ross-references: EMBL:X56370 ccession: \$12427 tatus: translation not shown	22AGCTGGTTAGCCATCATCTTAGCTGG
Notecule type: DNA (Residues: 1-101 < SA4>	DD 38 GGLYITPVALAKGGINMGCPTGGIYLGGGGIUITPMGCGIYILGIGGIYFFTGGI 58 QY 48 TGACTCTGATACCACATACACGCCGTCCTTCCAAGGC 84
status: translation not shown folecule type: DNA	58
<u>-</u>	RESULT 8 PH1279 IG heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-C; Species: Homo sapiens (man)
A;RoteCules: 1-101 <sa6> A;Residues: 1-101 <sa6> A;Cross-references: EMBL:X56371 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin homology F;18-101/Domain: immunoglobulin homology <imm></imm></sa6></sa6>	Cipate: 3.0-Sep-1993 #Bequence_revision 30-Sep-1993 #text_change 16-Aug-1996 CiAccession: PH1279 R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W. J. Exp. Med. 176, 1073-1081, 1992 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chromal Richems R
	A;Accession: PH1279 A;Molecule type: DNA A;Esidues: 1-102 < CAI> A;Esidues: 1-102 < CAI> A;Experimental source: adult PBL C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;19-102/Domain: immunoglobulin homology < IMM>
S12424 (1-101)	ις.
GCCGAGTCA	t Similarity: 45.28% Concues: ocal Similarity: 43.40% Mismatches: Match: 1ndels: 2 Gaps:
22	NOLAN463-2B.SEQ (1-84) x PH1279 (1-102) Qy 3 GGCGAGTCA21

Best Local Similarity: 43.40   Mismatches: 3   Query Match: 69.86   Indels: 2   2	Oy 48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84	A; Molecule type: DNA A; Residues: 1.102 <cai>A; Residues: 1.102 <cai <imm="" c;="" domain:="" f;19-102="" heterotetramer;="" homology="" immunoglobulin="" keywords:="" region;="" superfamily:="" v=""> Alignment Scores: Alignment Scores: Pred. No: Cores: Cor</cai></cai>	NOLAN463-2B.SEQ (1-84) x PH1272 (1-102)   GGGTATTAGC	Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70  RESULT 12  PH1282 Ig heavy chain V region (clone PBL13) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens C;Accession: PH1282 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron A;Reference number: PH1232; MUID:93018822; PMID:1402653 A;Recension: PH1282 A;Recension: PH1282 A;Recension: PH1282 A;Recension: H1282 A;Rece
	Ig heavy chain V region (clone PBL12) - human (fragment)  C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens C; Steession: PH1281 R; Cai, J; Humphries, C; Richardson, A.; Tucker, P.W. J; Exp. Med. 176, 1073-1081, 1992 A; Title: Extensive and selective mutation of a rearranged VHS gene in human B cell chron A; Reference number: PH1281 A; Accession: PH1281 A; Residues: 1-102 <cai>A; Residues: 1-102 <cai>A; Residues: 1-102 <cai>A; Residues: 1-102 <cai>CAII + Munnoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin homology <imm></imm></cai></cai></cai></cai>	Alignment Scores:	Oy 22AGCTGGTTAGCCATCATCTTGG 47  Db 38 GGlyTrpValArgGlnMetProGlyLeuGluTrpMetGlyIleIleTyrProGl 58  Qy 48 TGACTCTGATACCACATACAGCCGTCCTTCCAAGGC 84  [	C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996 C;Accession: PH1244 R;Cai, J.; Humphrises, C.; Richardson, A.; Tucker, P.W. J. Exp. Med. 176, 1073-1081 1992 A;Title: Excensive and selective mutation of a rearranged VH5 gene in human B cell chror A;Reference number: PH1232; MUID: 93018822; PMID: 1402653 A;Reference mumber: PH1232; MUID: 93018822; PMID: 1402653 A;Reference rumber: PH1232; MUID: 93018822; PMID: 1402653 A;Reference number: PH1232; MUID: 93018822; PMID: 1402653 A;Restance type: DNA A;Resta

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A; Title: Extensive and selective mutation of a rearranged VH5 gene in human 1A; Reference number: PH1232; MUID:93018822; PMID:1402653
A; Recession: PH1244
A; Molecule type: mRNA
A; Residues: 1-102 < CAI>A; Resperimental source: EBV-transformed CD5+ B cell [from adult PBL]
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 10-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1258
B;Cai, J; Humphries, C; Richardson, A; Tucker, P.W.
J. Exp. Med. 175, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B ce A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Residues: 1102 cCAI>
A;Residues: 1-102 cCAI>
A;Residues: 1-102 cCAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH126 K
S;Accassion: Jumphries, C:; Richardson, A:; Tucker, P.W.
J: Humphries, C:; Richardson, A:; Tucker, P.W.
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C; Keywords: heterotetramer; immunoglobulin P;19-102/Domain: immunoglobulin homology <IMM>
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Search completed: August 4, 2005, 19:02:37 Job time : 18.75 secs

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EMBL: U78801, AAD00293.1; --.
HSSP: P01751; INQB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q921C4 PRELIMINARY; PRT; 118 AA.
0221C4; 0221C4; 0221C4; 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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082KG0
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0686K9
0686S7
HV1B HUMAN
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091052
091043
0931W13
0931W13
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Q6GNX4
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InterPro; IPR003596; 1g_v.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity:
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                            OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1612378 seqs, 512079187 residues
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0921C4
0903H6
07TMT6
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HV52 MOUSE
091L83
091W11
06PF95
099LC4
HV0F HUMAN
HV0F MOUSE
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                 RESULT 3
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SECUENCE FROM N.N.

STRAID=CZECH II; TISSUE=Mammary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownerein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.M., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G.,

Ratesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ratesley M.W., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length human
                     9
                                          58
                                 1 CGGCCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG PMC; UNKNOWN 1.
SEQUENCE 474 AA, 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474
14
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                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                  474 AA.
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                                                                 61 ACATACAGCCCGTCCTTCCAAGGC 84
                                                                              :::|||:::
59 SerTyrThrGlnLysPheArgGly 66
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NOLAN463-2B.SEQ (1-84) x Q9Z1C4 (1-118)
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52.50%
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                                                                                                                                  PRELIMINARY;
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Best Local Similarity:
                                                                                                                                                                                        AU044919 protein.
                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                    Name-AU044919;
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STRAINE-205915.0; IISSUE-Testis;
STRAINE-2049374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata to
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium, the Right Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length oDNAs."; Nature 420:563-573 (2002).
                                                                                    1 CGGCCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:1700110L11 product:immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/67; TISSUE=Testis;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/60; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA.
                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                               78 HisTyrSerGlyLysPheGlnGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
NOLAN463-2B.SEQ (1-84) x Q8R3H6 (1-474)
                                                                                                                                                                                                                                                        61 ACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J, TISSUE=Testis;
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Query Match:
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DOMAIN
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Brownstein M.J., Usdin T.B., Foshiyuki S., Carninci P., Prange C.,

B. Brownstein M.J., WcKernan K.J., Abramson R.D., Mullahy S.J.,

B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rabesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
STRAIN=C57BL/6J; TISSUE=Testis;
Adachi J., Aizawa K., Akahira S., Pukuda S., Fukuda H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukuda M., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Furuno M.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Acazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Anchima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BEMBL; AKO07163; BAB24877.1; -.
RINEFPRO; IPR00120; 1G7J.
RINEFPRO; IPR00120; 1G7J.
RINEFPRO; IRR07110; Ig-like.
RINEFPRO; SMART; SM00406; IGY: ICY: ICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             874DDF7BD98BD7B2 CRC64;
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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65 AsnTyrAsnGlyLysPheLysGly 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.-
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 111 AA; 11976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.49
76.70
60.00$
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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DB:
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59 ArgProGlyLysGlyLeu---GluTrpIleGlyArgValTyrProGlyAspGlyAspThr 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I. MISCELLANEOUS: This germline gene belongs to a set of closely related genes that could encode V regions of NPb antibodies.

PIR, A02023, HWRS02.

PDB; 10NR H=20-117.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Ffam; PR00407; ig; 1.

PROSITE; PS50835; IG_LIKE; 1.

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region 102. Framework-1. Complementarity-determining-1. Framework-2.
                                                                                                                                                   EMBL, BC053409, AM53409.1;
HSSP, P01820, 1G7J
HSSP, P01820, 1G7J
HSSP, P01820, 1G7J
HTGFPC, IPR00710, IG-like.
InterPro; IPR033006, Ig_MHC.
InterPro; IPR03306, Ig_W.
Ffam; PP07654, C1-set; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS00835, IG_LIKE, 5.
PROSITE; PS00835, IG_LIKE, 5.
SRQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;
                                                                                                                  Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              614
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                                                                SEQUENCE FROM N.A. STRAIN-C57BL/6NCr; TISSUE-Hematopoietic Stem Cell;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Appary chain V region 102 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA.
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78 AsnTyrAsnGlyLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOLAN463-2B.SEQ (1-84) x Q7TMT6 (1-614)
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75.70
60.00%
40.00%
51.15%
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54
68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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P01750;
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Percent Similarity:
Best Local Similarit
                                      Percent Similarity:
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SEQUENCE
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Q91WT1;
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                                                                                                                                                                                                                                                                                                                                                                                             Q9JL83
  Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                         1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2; Yancopoulos G.D., Alt F.W.; Provedopmentally controlled and tissue-specific expression of unrearranged VH companies."; Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region VH558 A1/A4.
Framework-1.
    Complementarity-determining-2. Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-1
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                                                                                   12867 MW; 740A65DD851FCA8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12971 MW; 8B0BC138856DFC9D CRC64;
                                                                                                                                             117
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Matches:
Conservative:
Mismatches:
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01-JAN-1998 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Paevy chain V region VH558 A1/A4 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA.
                                          By similarity
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Gaps:
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AsnTyrAsnGlnLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; iGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M13787; AAA38499.1; -. PIR; AO2029; HVMSA1. HSSP; P01820; 1G7J. InterPro; IPR007110; IG-like. InterPro; IPR003596; IG_V.
                                                                                                                                             2.72
74.70
60.00%
43.33%
50.47%
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117
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41 1
117 AA;
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117
117 AA;
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                                                                                                                                                                                                           Best Local Similarity:
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                                                                                                                                                                                      Percent Similarity:
                                                                                                                          Alignment Scores:
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DOMAIN
DISULFID
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DISULFID
                                                              NON TER
SEQUENCE
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DB:
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                                                                                                                                                                                       1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1128/IAI.68.10.5803-5808.2000; Malkiel S., Liao L., Cunningham M.W., Diamond B.; Malkiel S., Liao L., Cunningham M.W., Diamond B.; T.Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
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1117
113
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13
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                       110 AA.
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                                                                                                                               NOLAN463-2B.SEQ (1-84) x HV52_MOUSE (1-117)
                                                                                                                                                                                                                                       61 ACATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                  |||:::|||
78 LysTyrAsnGluLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrTyrAsnGlyLysPheLysGly 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with cardiac myosin.";
Infect. Immun. 68:5803-5808 (2000).
EMBL. PATOGOD3; AAF69321.1;
HSSP, POT751; NNOB.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-v.
SMART; SM00406; IGV; I.
PROSITE; PS50835; IG_LIKE; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
MEDLINE=20448942; Pubmed=10992488;
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73.70
56.67%
43.33%
2.72
74.70
56.67$
43.33$
50.47$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                        Best Local Similarity:
Query Match:
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NCBI_TaxID=10090;
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                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481
13
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0
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ACATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||::: ||||
78 LysTyrAsnGluLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOLAN463-2B.SEQ (1-84) x Q91WT1 (1-481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC013490; AAH13490.1; -. HSSP; P01751; 1A6W. Pfam; PF07654; C1-set; 2.
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
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73.70
60.00%
43.33%
49.80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
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                                                 musculus (Mouse).
                                   Igh-VJ558 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                              NCBI_TaxID=10090;
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Percent Similarity:
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Q6PP95;
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DB:
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TRAINSCEACH II; TISSUE=Mammary tumor;

MEDLINE=2238257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg N.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Schmeen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hopkins R.P., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Acharsein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S. K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S. K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S. K., Muzny D.M., Sodergren E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

Jones S.J., Marra M.A.,

Thencration and initial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more than 15,000 full-length human and mouse control and sintial analysis of more tha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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59 ArgSerGlyGlnGlyLeu---GluTrpIleAlaArgIleTyrProGlyThrGlySerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BCO57672, AAHS7672.1; -- HSSP; PO1865; 1KBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 464 AA; 51096 MW; 5B837464D85A1888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464
113
9 9 9 9 0
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Last sequence update)
Last annotation update)
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Mismatches:
Indels:
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Matches:
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_C1.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_N.
InterPro; IPR003596; IG_N.
InterPro; IPR003596; IG_N.
InterPro; IPR00406; IG, 2.
SWART; SW00406; IG, 1.
IPROSITE; PS50835; IG_LIKE; 4.
IPROSITE; PS02909; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CZECH II; TISSUE=Mammary tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:::|||
TyrTyrAsnGluLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.12
72.70
60.00%
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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125 AA.

STANDARD;

HUMAN

84 85

61 ACATACAGCCCGTCCTTCCAAGGC ||||||| TyrTyrSerGluLysPheLysGly

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MEDLINE=86203277; PubMed=3084950; DOI=10.1016/0161-5890(86)90039-8;
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kojima Bookoly, remarka S., Ono T.;

Kojima M., Koide T., Odani S., Ono T.;

"Amino acid sequence of the variable region of heavy chain in immunoglobulin. (Mot) having unusual papain cleavage sites.";

Mol. Immunol. 23.169-174 (1986).

PIR; A02025; HVHUWO.

HSSP; PO1751; 1A6W.

GO; GO: 0003537; Frantigen binding; NAS.

GO; GO: 0003557; Frantigen binding; NAS.

InterPro; IPR00710; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct protein sequencing; Immunoglobulin V region. DOMAIN 1 98 V segment.
                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-I region Mot.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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SEQUENCE
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                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Nammary tumor;

MEDLINE=233825; PubMed=1247931; DOI=10.1073/pnas.242603899;

MEDLINE=233825; PubMed=1247931; DOI=10.1073/pnas.242603899;

A strauberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A stachul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhat N.K.,

A stapleton M.; More T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Murny D.M., Sodesynen B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Minting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Green Eastlon and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SECUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Mammary tumor;

STRAIN=FVB/N; TISPUE-MAMMARY TISPUE-MAMMARY TIDA.

STRAIN=FVB/N; TISPUE-MAMMARY TIDA.

STRAIN-FVB/N; TISPUE-MAMMARY TIDA.

STRAIN-FVB/N; TISPUE-MAMMARY TIDA.

STRAIN-FVB/N; TISPUE-MAMMARY TIDA.

STRAIN-FVB/N; TISPUE-MAMMARY TISPUE-MAMMA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463
113
110
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches:
Conservative:
Mismatches:
Indels:
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43.33$
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Pred. No.:
Score:
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DB:
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By similarity. V segment. D segment. J segment.

125 125 125

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61
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                                                                                                                                                              42 GlyArg----GlyLeu---GluTrpMetAlaValValHisProSerAspArgThrT
                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
13579 MW; F4C4285D6DF0C8EA CRC64;
                                   125
12
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7
7
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                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                21-JJJ-1986 (Rel. 01, Created)
21-JJJ-1986 (Rel. 01, Last sequence update)
05-JJJ-2004 (Rel. 44, Last annotation update)
heavy chain V region 3 precursor.
Name=1gh-VJ558;
                                                                                                                                                                                                                                                                            117 AA
                                                                                                 Gaps:
                                                                                                                         NOLAN463-2B.SEQ (1-84) x HVIF_HUMAN (1-125)
                                                                                                                                                                                                                      hrTyrGlyProArgSerGln 65
                                                                                                                                                                                                  62 CATACAGCCCGTCCTTCCAA 81
                                    18.7
68.20
53.12%
37.50%
                                                                                                                                                                                                                                                                            STANDARD;
  AA;
                                                                         Best Local Similarity:
                                                            Percent Similarity:
                         Alignment Scores:
                                                                                                                                                                                                                                                                            HV05 MOUSE
                                                                                                                                                                                                                           59
                                                                                      Query Match:
                                      No.:
                                                                                                                                                                                                                                                     RESULT 12
HV05_MOUSE
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1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC

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STRAIN=C57BL/6;
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                                                                                                                                                                                                                                                                                                                                                                   Q6GMX8
                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                 Score:
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 STIRBBRREFFS
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-1- MISCELLANEOUS: This germline gene belongs to a set of closely related genes that could encode V regions of NPb antibodies.
        STRAIN=CS7BL/6;
MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazia; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
VH186.2-J-C mu protein (V304-D-J-C mu protein) (Fragment)
Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region 3. Pramework-1. Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                        427C861C53975EDC CRC64;
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122
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||:::
78 HisTyrAsnGlnLysPheLys 84
                                                                                                                                                                                                                                                                         PFam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                 PINE, A02031; HYMS3.
HSSP; P01810; ZFBJ.
MGD; MGI:96486; IGh-VJ558.
INTERPRO; IPRO07110; IG-like.
InterPro; IPR003596; IG-v.
                                                                                                                                                                                                                                                                                                                                                                                                                        13016 MW;
                                                                                                                                                                                                          EMBL; J00536; AAA38605.1; -.
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67.70
58.62%
41.38%
45.74%
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54
68
85
117
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FROM N.A.
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Best Local Similarity:
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SEQUENCE FROM N.A.
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Pred. No.:
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SEQUENCE
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CTISSUB-Primary B-Cells;

XX STRUB-Primary B-Cells;

XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Rausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Detchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.

Hypothetical protein.

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069912; BAB63928.1; -.
EMBL; AB069914; BAB63930.1; -.
EMBL; AB069914; BAB63930.1; -.
EMBL; AB069914; BAB63930.1; -.
ENRL; AB06914; BAB63930.1; -.
SNART; SM00406; IGv; 1.
PROSITE; PS0835; IG_LIKE; 1.
NON TER 143 143
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073764; AAH73764.1; -.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           143
110
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 AsnTyrAsnGlnLysPheLysGly 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        29.8
66.70
56.67%
40.00%
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
023-D-J-1gG1 protein (Fragment).
Name=V23-D-J-1gG1;
Nus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscularia; Rodentia; Sciurognathi; Muridae; Musinae; Musina
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STRAIN=CS7BL/6;
KOZONO Y., KOZONO H., Azuma T.;
KOZONO Y., KOZONO H., Azuma T.;
The higher density hapten Ag stimulates strong signal to B (Submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069864; BAC54573.1; -.
HSSP; PO1751; 1A6V.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE; 1.
InterPro; IPR003599; IG.
InterPro; IPR003100; Ig-like.
InterPro; IPR003100; Ig-like.
InterPro; IPR003006; Ig-C1.
InterPro; IPR003006; Ig-Mc.
InterPro; IPR003595; Ig-C1.
InterPro; IPR003506; Ig-Wc.
InterPro; IPR003506; Ig-Wc.
InterPro; IPR00400; Ig; 2.
IPR00400; Ig; 2.
IPR00400; IG; 2.
IPR00400; IG; 1.
IPR051TE; PS50835; IG-LIKE; 2.
IPR051TE; PS50835; IG-MC; UNKNOWN_1.
IPRO51TE; PS50836; IG-MC; UNKNOWN_1.
IPRO51TE; PS00290; IG-MHC; UNKNOWN_1.
IPRO51TE; PS00290; IG-MHC; UNKNOWN_1.
IPR051TE; PS00290; IG-MHC; UNKNOWN_1.
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Matches:
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1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTTATCCTGGTGACTCTGATACC 60

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4, 2005, 19:01:29
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56 AsnTyrAsnGluLysPheLys 62
                                               61 ACATACAGCCCGTCCTTCCAA 81
                                                                                                                          Search completed: August
Job time: 85.75 secs
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Total number Minimum DB Maximum DB

Searched:

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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulator; immunosublatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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Human bra
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Human ant
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scFv Ab12
Anti-rhes
 Human ger
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Lymphoma
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Antibody
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Abo27107
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Adb75646
Adf10104
Adf101950
Adf101950
Aab011959
Aab011959
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Aab011955
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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ADA89246
ADK17418
ADG42840
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ABR42859
ABW02445
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AAB01949
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AAB01953
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ADA89274
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ADF09942
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AAY34299
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2000US-0240816P.
2001US-0276248P.
2001US-0277379P.
2001US-0293499P.
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16-MAR-2001;
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 ABP45310;
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    Abp45310 Human BLy
Adg95137 Single ch
Abp4982 Human BLy
Adg95809 Single ch
Abp4943 Human BLy
Adg95770 Single ch
Adg95770 Single ch
Adw62794 Amino aci
Aay65594 Multiple
Abg91903 Human Fv
Abg91903 Human ant
                                                                                                    August 4, 2005, 19:02:48; Search time 114 Seconds (without alignments) 549.607 Million cell updates/sec
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                5.1.6
Compugen Ltd
                                                                         protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                2105692 seqs, 386760381 residues
                GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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11-MAR-2004

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E Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell through the control of the invention and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency (GVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP41228 represent the antibodies and fragments of the antibodies described in the method of
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                                                            Lymphocyte Stimulating polypeptides, useful for the sut of cancers and immune disorders.
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Vaughan T, Hilbert D;
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Choi GH,
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20.63%
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Barash SC,
                                                              Antibodies against B
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Query Match:
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this interitor letaces to nover anticonstruction of the tumour checks and encodes a protein that is a member of the tumour checks factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable chary (DTS region that immunospecifically bind to a polyectide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders can conform or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysatchenia gravis and multiple sclerosis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and theumatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and crivities such as anticheumatic, antiallergic and cytostatic. This artificial antichlaumatory, antiasthmatic, antiallergic and cytostatic. This cinvention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format of directely from WIPO at ftp.wipo.int/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                       antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoroid arthritis; ADDS; leukaemia; carcinoma; lymphoma; antirtheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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19-DEC-2001; 2001US-0340817P.
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                        130 GlySerGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
                                                                                                                                                                                                                       This invention describes novel antibodies that immunospecifically bind to
                                                       90 ThralavalTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
                                                                                                               110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
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SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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16-MAR-2001;
21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthriti; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody that immunospecifically binds BLyS SeqID 993
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Conservative:
Mismatches:
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                                                               Sequence 250 AA;
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proliferation and differentiation. Specifically, it refers to single chain antibody molecules (screw) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polyapptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders uncluding myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and Lymphoma. Accordingly, they can be described as exhibiting various ctivities such as antirheumatic, antiallergic and cytostatic. This antinflammatory, antiasthmatic, antiallergic and cytostatic. This invention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format circlely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATCAATGATAGTGGAAGCACCAACTACAACCGGTCTCTCAAGAGTCGGGCG----- 54
                                                                                                                                                                                                                                                                                                                                                                                                                   250
23
123
123
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Matches:
Conservative:
Mismatches:
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80.77%
76.92%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2010US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P.

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, theumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (evi) and acquired immunodeficiency sudments of the antibodies described in the method of
                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis, asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirtheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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             Hilbert D;
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20
1
2
2
1
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Matches:
Conservative:
Mismatches:
Indels:
               Vaughan T,
                                                                                                                                   Claim 1; Page 1540-1541; 3148pp; English
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               Choi GH,
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|SerGlnAspThrSerAsn 75
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                 Barash SC,
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
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                 Ruben SM,
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to Chromosome 1344 and encodes a protein that is a member of the tumour chromosome 1344 and encodes both in vivo and in vitro B cell necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single contains that is munospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The chary CDR3 region that immunospecifically bind to a polypeptide, or fragment invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the abstrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysathenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This attinflammatory, antiasthmatic, antiallergic and cytostatic. This curvention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format of the printed specification, but was obtained in electronic format of the printed specification, but was obtained in electronic format of the such are all the such as a single chain as electronic format of the printed specification, but was obtained in electronic format of the printed specification, but was obtained in electronic format of the printed specification, but was obtained in electronic format of the such as a supplementations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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19-DEC-2001; 2001US-0340817P.
                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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253
20
1
3
3
     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
     0.00328
93.80
80.77$
76.92$
67.00$
                               Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                      Query Match:
DB:
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DELETED1 (1-81) x ADG95770 (1-253)

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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG-----
                                              55 AGTCAGGATATTAGCAGC 72
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                       셤
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2

AAW62794 standard; peptide; 80 AA RESULT 7

AAW62794;

(first entry) 23-SEP-1998 Amino acid sequence of a human antibody fragment.

Human; immunoglobulin; Ig; transgenic; non-human mammal; inactivated endogenous Ig locus; B-cell development; human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene; kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa; production; antibody. 

transgenic Xenomice, created using the method of the invention. The predictation describes a transgenic non-human mammal which has genome predictation describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin [Ig] locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in modified genome also here, and human N-H genes and an inserted human Appa Genes, human D-H genes, and human V-H genes and an inserted human kappa light chain Ig locus in germline configuration, the human kappa light chain Ig locus in germline configuration, the human kappa light chain Ig locus where the number of V-H and V-kappa genes, nere the number of V-H and V-kappa genes inserted are selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e-g. when exposed to human antibodies when exposed to particular antigens e-g. when exposed to human lL-8, EGFR or TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha respectively New transgenic non-human mammals - having an inactivated immunoglobulin locus and a near complete human immunoglobulin locus, used for production Mendez M, Klapholz S, Disclosure; Page 71; 128pp; English. Jakobovits A, Kucherlapati R, 97WO-US023091 96US-00759620 (ABGE-) ABGENIX INC. of human antibodies. WPI; 1998-333314/29. Sequence 80 AA; Homo sapiens. WO9824893-A2. 03-DEC-1997; 11-JUN-1998. 

0611190 Length: Matches: Conservative: Mismatches: Indels: 0.00354 92.40 74.07**\$** 70.37**\$** 66.00**\$** Percent Similarity: Best Local Similarity: Alignment Scores:

DELETED1 (1-81) x AAW62794 (1-80)

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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60 61 GATATTAGC 69 ò ઠ

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AAY05694 standard; protein; 97 AA 19-JUL-1999 (first entry) RESULT 8
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Multiple sclerosis patient CSF B-cell VH region (clone 4d76)

Multiple sclerosis, cerebrospinal fluid, CSF; B-cell, heavy chain variable region; VH gene, somatic hypermutation;

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from DNA of dominant clone 4d76 of B-cells taken from the crebrospinal from DNA of dominant clone 4d76 of B-cells taken from the crebrospinal fluid (CSF) of a multiple sclerosis (WS) parient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19). Differences in nucleotide and predicted amino acid (see AAX05691-94) sequences were compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded e-cells from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that havd undergone antigen selection. This finding implicates an important pathogenic pathway for
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This sequence represents a heavy chain variable region (VH) as predicted Determination of B-cell clonality by amplification or enzymatic B-cell clonality; RA gene; diagnosis; human. RA" RA" note= "replaces Phe of RA" æ Æ note= "replaces Asn of RA" Ŗ. Leu of RA" /note= "replaces Arg of RA" Phe of RA" Æ. note= "replaces Glu of Gly of οŧ note= "replaces Gly of Gly of Ser of . GGC-Location/Qualifiers 1. .30 /label= FR1 note= "encoded by note= "encoded by Disclosure, Fig 9D; 67pp; English, note= "replaces note= "replaces note= "replaces note= "replaces note= "replaces note= "replaces 97CA-02216595. 97CA-02220245. 'label= CDR2 98WO-CA000873 31. .36
/label= CDR1 57. .97 /label= FR3 77. .50 |abel= FR2 99. . WPI; 1999-276985/23. N-PSDB; AAX25318 Misc-difference X NIO (/XNIO) 17-SEP-1998; WO9915696-A1 04-NOV-1997; Homo sapiens 01-APR-1999 19-SEP-1997;

The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (ScFv) or a disulfide Fv (GsFv) or The peptide, optionally in association with or attached, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia. 68 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60 Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy development of demyelination in CNS of MS. The invention provides Levanon A; Human Fv molecule hypervariable region related peptide #87. Szanton E, 97 113 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: Guy R, Lipschitz O, Claim 13; Page 193; 232pp; English. ABG78212 standard; protein; 97 AA. (BIOT-) BIO-TECHNOLOGY GEN CORP. 31-DEC-2001; 2001WO-US049440. 29-DEC-2000; 2000US-00751181. DELETED1 (1-81) x AAY05694 (1-97) 0.00375 92.40 74.07% 70.37% 66.00% (first entry) Lazarovits J, 70 61 GATATTAGC 69 WPI; 2002-619166/66. ---ileser Percent Similarity: Best Local Similarity: Ŗ WO200259264-A2. 15-NOV-2002 Homo sapiens. Alignment Scores: Sequence 97 01-AUG-2002 Hagai Y, I Plaksin D, ABG78212; -20 69 Query Match: DB: cells. .. 02 RESULT 9 8888888 g 엄 ò ò

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the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one
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                                                                                                                                                                                                                                                                                                         GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG
                                                                                                                                                                                                                                                                                                                       Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
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Levanon A;
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Amit B, Kooperman L,
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epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thromboais, restenosis, metastaais, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet of tumour or leukaemia cells, for increasing the susceptibility of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.
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The invention describes a method of making a humanised antibody, comprising making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis of the selection, for humanisation. The method is useful for making a humanised antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human ramework sequences to support non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparison framework sequences. The antibody has high affinity and low immunogenicity without need for comparison framework sequences between non-human and human antibodies. This sequence represents a human heavy chain variable region gene segment used in the antibody library; CD1 region; CD2 region; VH region; VL region; immunoglobulin; CD3 region; TM1 scFv; human. Human protein relating to the invention SEQ ID NO:55. 0 0 1 1 9 2 Length:
Matches:
Conservative:
Mismatches:
Indels: Ξ ADB75646 standard; protein; 97 AA. creation of humanised antibodies Okui 22-NOV-2002; 2002WO-JP012236. 22-NOV-2001; 2001JP-00358602 DELETED1 (1-81) x ABO27107 (1-97) 0.00375 92.40 74.07**%** 70.37**%** 66.00**%** (first entry) Takayanagi A, 69 70 WPI; 2003-449818/42. 61 GATATTAGC ---Ileser (UYKE-) UNIV KEIO. Percent Similarity: Best Local Similarity: WO2003044198-A1. Sequence 97 AA Homo sapiens. 04-DEC-2003 Alignment Scores: 30-MAY-2003 Shimizu N, ADB75646; 69 Query Match: DB: RESULT 12 ADB75646

ADB7 ADB75646

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XXX ADB7

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Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                      The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CD1 and CD2 regions of the WH or VL region of immunoglobulin gene and a fragment containing the CD3 region by PCR, respectively, producing WH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-cell; malignant; immunoglobulin; immunoglobulin variable region; Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor;
contamination from unexpressible ones, useful as tool in
             proteomics and e.g. for diagnosis and treating various diseases
                                                                                                                                                                                                                                                                                                                           Lymphoma related immunoglobulin variable region F5.
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                                               Disclosure; Page 101; 108pp; Japanese.
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normal

Highly stable artificial antibody libraries with super-repertory and

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The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as presence of a glycosylation site, also described: (l) treating a patient suffering from or at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor cinhibiting glycosylation of the Ig variable region of the B cell receptor inheraction between lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (8) has cytosytation inhibitor. The method is useful in classifying a B-cell as glycosylation inhibitor. The method is useful in classifying a B-cell as melicament or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence exemplification of the present invention.
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              Disclosure; Fig 4; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003074679-A2.
                                                                                                                                                                                                                                                                                                                            Sequence 97 AA;
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DB:
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, could not a patient. The present sequence is an antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATCAATCATGGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
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Indels:
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                            Example 6; Fig 16a; 135pp; English
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29-MAY-2002; 2002US-0384197P.
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66.00%
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                                                                                                                                                                                                                                                                                         Sequence 97 AA;
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
Example 16; Fig 40a; 135pp; English.
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70.37\$	800.99	7
Sest Local Similarity:	nery Match:	B:

97 119 0	
Length: Marches: Conservative: Mismatches: Indels: Gaps:	
0.00375 92.40 74.078 70.378 66.008	150 (1-97)
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	DELETED1 (1-81) x ADF10150 (1-97)

61 GATATTAGC 69 ---IleSer 70 69 ð g ð

Search completed: August 4, 2005, 19:34:16 Job time : 120 secs

OM nucleic

Run on:

Sequence:

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APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESSONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                            Sequence 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6
Sequence 3
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence S
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US-09-802-096-5
US-09-802-077-5
US-09-371-276-835
US-09-371-276-835
US-09-371-276-835
US-09-371-16
US-08-428-197-16
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US-09-490-138-091A-142
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ZIP: 02110-2804
COMPUTER READDABLE DISKETTE
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FastSCD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR.1996
PRIOR APPLICATION DATA:
PRILING DATE: 17-MAR.1996
PRIOR APPLICATION NUMBER: PT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
RGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFRX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 118, Application US/08545809A; Patent No. 6096878; GENERAL INFORMATION:
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       Command line parameters:

-QCOMMand line parameters:
-QCOMMANDELFframe+ n2b.model -DEV=xlp
-Q=/cgn2_1/USFTQ-gpool_p/NOLAN463-3A/runat_04082005_120126_18820/app_query.fasta_1.263
-Q=/cgn2_1/USFTQ-gpool_p/NOLAN463-3A/runat_04082005_120126_18820/app_query.fasta_1.263
-DES=188ued_Patents_AA -QPMT=fastan -SUPFIX=rai -MINNATCH=0.1 -LOOPCIS=0
-LOOPEXT=0 -UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM+ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-NOLAN463-3A @CGN 1 1 46 @runat 04082005 120126_18820 -NCPU=6 -ICPU=3
-NO MAMP -LANCEGUERY -RGS=0 -MAHT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
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                                                                                                                                                                          August 4, 2005, 19:25:09; Search time 30 Seconds (without alignments) 403.105 Million cell updates/sec
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11: /cgn2_6/ptodatca1/iaa/5A_COMB.pep:*
12: /cgn2_6/ptodatca1/iaa/5B_COMB.pep:*
13: /cgn2_6/ptodatca1/iaa/6A_COMB.pep:*
14: /cgn2_6/ptodatca1/iaa/6B_COMB.pep:*
15: /cgn2_6/ptodatca1/iaa/PCTUG_COMB.pep:*
16: /cgn2_6/ptodatca1/iaa/PCTUG_COMB.pep:*
17: /cgn2_6/ptodatca1/iaa/PCTUG_COMB.pep:*
18: /cgn2_6/ptodatca1/iaa/PcCTUG_COMB.pep:*
18: /cgn2_6/ptodatca1/iaa/backfiles1.pep:*
18: /cgn2_6/ptodatca1/iaa/backfiles1.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                              - protein search, using frame_plus_n2p model
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US-08-793-450-4
US-09-203-768A-2
US-08-793-450-8
US-09-372-425A-6
US-09-490-070A-25
US-09-490-153-25
US-09-490-153-25
US-08-446-151-5
US-08-446-151-5
US-08-466-151-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      992.4
992.4
992.4
992.4
884.4
84.4
84.4
811.8
80.7
                                                                                                                                                                                                                                                                                                        Perfect score:
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Result

Minimum DB Maximum DB

142, App 55, Appl 19, Appl 19, Appl 19, Appl 65, Appl 65, Appl 66, Appl 67, Appl 77, Appl 78, Appl 78, Appl 78, Appl 79, Appl 70, Appl 70, Appl 70, Appl 71, Appl 71, Appl 72, Appl 73, Appl 74, Appl 75, Appl 76, Appl 77, Appl 77, Appl 78, Ap

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Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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DB:
                                                                                Query Match:
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                                                                                                                                                                                                                                                                                                 APPLICANT: EDELMAN, LENA
APPLICANT: MACGARITTE, CHRISTEL
APPLICANT: MACGARITTE, CHRISTEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STRRET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
                                                                                                                                                   116
119
11
11
0
                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660-118-0 PCT
                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                DELETED1 (1-81) x US-08-545-809A-118 (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
ATTOLING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0
TELECOMMUNICATION INFORMATION:
TELECPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               0.000397
92.40
74.07%
70.37%
66.00%
               SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 123 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-4
                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                            88 ---IleSer 89
                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: VA
COUNTRY: USA
ZIP: 22202
                                                                                   ; MOLECULE TYPE:
US-08-545-809A-118
                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-793-450-4
                                                                                                                                                                                                               Query Match:
DB:
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Sequence 2, Application US/09203768A

| Sequence 2, Application US/09203768A
| Sequence 2, Application US/09203768A
| Sequence 2, Application US/09203768A
| Sequence 2, Application US/09203768A
| Sequence 2, Application US/09203768A
| Septimization US/09708A
| APPLICANT: Huse, William D.
| APPLICANT: Huse, William D.
| APPLICANT: Huse, William D.
| TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
| TITLE OF INVENTION: Of USe
| TITLE OF USE OF USE
| TITLE OF USE OF USE
| SEQ ID NOS: B
| SEQ ID NOS: B
| LENGTH: 139
                                                                                                                                                                                        1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BDELMAN, LENA
APPLICANT: MARGARITTE,
APPLICANT: MARGARITTE,
APPLICANT: GHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: D.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
CREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
119
10
0
    123
119
119
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                         Gaps:
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                                                                                                                                                 DELETED1 (1-81) x US-08-793-450-4 (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 8, Application US/08793450 ; Patent No. 6312690
  0.000405
92.40
74.07%
70.37%
66.00%
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92.40
74.07$
70.37$
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                                                                                                                                                                                                                                                                                                              69 ---ileser 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-203-768A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GATATTAGC 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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US-08-793-450-8
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Query Match:
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119
11
6
0
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APPLICANT: Sherie L. Morrison
APPLICANT: Ramon Montano
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE S: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 1067
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
CHORDON NOT COMPUTER: MS WORD
CHORDON NOT COMPUTER: MS WORD
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compactible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                 APPLICATION NO..._
FILING DATE: 03-MAR-1997
CLASSIPRICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY OBLON, NORMAN F.
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 660-118-0 PCT
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3220
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: linear
TYPE: linear
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELETED1 (1-81) x US-08-793-450-8 (1-472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 6, Application US/09372425A; Patent No. 6475749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.000659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.40
74.07$
70.37$
66.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||
88 ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGGGAGTCAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/09025769B

Sequence 25, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Back, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ilag, Vic

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STREET: 1251 Avenue of the Americas

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPRENTING SYSTEM: PC-006/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-ETB-1998

FILING DATE: 18-AUG-1995

ATTORNEY APPLICATION NUMBER: 27,794

RESISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                      510015-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELETED1 (1-81) x US-09-372-425A-6 (1-429)
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 5100
TELECOMMUNICATION INFORMATION:
FELEPRORE: (310) 788-5000
TELERAX: (310) 788-5000
TELERAX: (310) 788-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00305
87.40
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.07$
66.67$
62.43$
                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 ---IleSer 89
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-025-769B-25
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Pred. No.:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION UNMBER: 31,298
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37,299
TELECOMMUNICATION: (2022) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pack, Peter
Ilag, Vic
Ge, Limino
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                               118
118
12
6
6
                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                      Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TELEPHONE: (212)596-9000
TELEPAX: (212)596-90900
INPORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid STRANDEDNESS:
TOPPLOGY: linear
NOLECULE TYPE: protein
US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                               84.40
70.37$
66.67$
60.29$
                                                                                                                                                                                                               0.0049
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 --- ileser 70
                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-09-490-070A-25
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No.:
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50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
                                                                                                                                                                                                                                                                                    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDUUM TYPE: Floppy disk

COMPUTER: I BW PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAWE: James F. Haley, Jr., EEG.

REGISTRATION NUMBER: MORPHO/5

TELECOMMUNICATION NUMBER: MORPHO/5

TELECOMMUNICATION NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                  118
118
2
6
6
                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                   Indels:
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                            DELETED1 (1-81) x US-09-490-070A-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
;
TOPOLOGY: linear
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                     84.40
70.37%
66.67%
60.29%
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                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                   Alignment Scores:
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TOPOLOGY:
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Query Match:
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                                                                                                                                                                 1 GARATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: E9 5 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Janes F. Halley, Jr., ESQ.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INDRER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
                 118
118
12
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18
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               Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                 Gaps:
                                                                                                                                DELETED1 (1-81) x US-09-490-153-25 (1-118)
                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09490324
Patent No. 6826422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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                                84.40
70.37$
66.67$
60.29$
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STATE: New York
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                                                                                                                                                                                                                                61 GATATTAGC 69
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                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Alignment Scores:
Pred. No.:
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Pred. No.:
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US-09-490-324-25
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
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APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCES: 145
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FaseESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/TOCKET NUMBER: 06501/004001
TELEPHONE: 617-542-8906
TELERX: 200154
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                                                          DELETED1 (1-81) x US-09-490-324-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                        Sequence 137, Application US/08545809A; Patent No. 6096878; GENERAL INFORMATION:
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amino acid
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62.50%
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60.29%
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity:
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STATE: MA
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Alignment Scores:
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US-09-802-096-5
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ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
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118
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardiau, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELETED1 (1-81) x US-08-466-151-5 (1-130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0162
80.70
47.92%
37.50%
57.64%
89 SerValAspThr 92
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US-08-466-151-5
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GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Paresta, Leonard G.
TITLE OP INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended,
TITLE OP INVENTION: Mothers: US/09/802,096
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 1995-03-18
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PELICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-08-14
PRIOR PILING DATE: 1922-08-14
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1991-08-14
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72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                           APPLICANT: Jardieu, Paula M.
APPLICANT: Dresta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2CID.
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILING DATE: 1995-03-15
PRIOR PILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 5-
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                                92 AlaThrTyrTyrCysAlaTrpVal 99
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78
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                                                                                                                            US-08-466-163B-5; Sequence 5, Application US/08466163B; Patent No. 6329509
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Patent No. 6685939
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80.70
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Best Local Similarity:
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Sequence 5, Application US/09802077

Batent No. 6699472

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Dardieu, Paula M.

TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: POT18P2C2US

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1992-03-15

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-06-07

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR PILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

LEMEGTH: 130

"WUNBER DATE: 130
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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57.64%
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                                                    ; ORGANISM: Mus musculus
US-09-802-096-5
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US-09-802-077-5
NUMBER OF SEQ ID NOS:
SEQ ID NO 5
LENGTH: 130
                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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US-09-802-077-5
                                          TYPE: PRT
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is Sequence 815. Application US/09471276
; Sequence 815. Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CP1
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: 09/057,719
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER PILING DATE: 1998-04-08
; EARLIER FILING DATE: 1998-04-08
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SEQTWARE: Patent.pm
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Job time : 32 secs
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ORGANISM: Homo sapiens
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Sequence 128, App
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TILLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TILLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TILLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PRILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

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-MODEL=trame+ n.D2p_model - DEV=xlp
-Q=/cgn12 1/USFTQ-gpool p/NOLAN463-3A/runat_04082005_120128_18886/app_query.fasta_1.263
-Q=/cgn2 1/USFTQ-gpool p/NOLAN463-3A/runat_04082005_120128_18886/app_query.fasta_1.263
-DB=Published Applications AA -QFWT=fastan -SUPFIX=Tapb -MINMATCH=0.1
-LOPDEXT=0 -LOPDEXT=0 -LOTNITS=bits START=1 - END=-1 - MATKTS=biosum62
-TRANS=human40.cdi -LIST=45-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-THR_NN=0 -ALIGN=15 -MODE=LOCAL_OUTFWT=pto -NORM=ext - HEAPSIZES=500 -MINLEN=0
-THR_NN=0 -ALIGN=15 -MODE=LOCAL_OUTFWT=pto -NORM=ext - HEAPSIZES=500 -MINLEN=0
-NAXLEN=200000000 -USER=NOLAN463-3A @CGN 1 1 199 @runat - OSPBLOCK=100
-NCPU-6 - ICPU-3 -NO MAAP -LARGEQUERY - NEG SCORES=0 - MAIT - DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPEXT=0.1
-FGAPOP=6 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
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| Cgn2_6/ptodata1/Ipubpaa/USS0_NEW_PUB.ppp:"
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                           protein search, using frame_plus_n2p model
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NUMBER OF SEQ ID NOS: 3239; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 1321; LENGTH: 249
                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321
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Sequence 12, Application US/10898408

Sequence 12, Application US/10898408

Publication No. US20050058642A1

GENERAL INFORMATION:
APPLICANT: GALIBERT, Laurent J.
APPLICANT: TAN, Wei
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-A

CURRENT FILING DATE: 2004-07-23

PRIOR FILING DATE: 2003-07-25

NUMBER: OF SEQ ID NOS: 13

SOFTWARE: Patentin Version 3.2

SEQ ID NO 12

LENGHA: 115
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; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321
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| Sequence 954, Application US/09880748
| Publication No. US20030059937A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| FILE REPERBENCE: PF23
| CURRENT APPLICATION NUMBER: US/09/880,748
| CURRENT FILING DATE: 2001-06-15
| PRIOR PELICATION NUMBER: 60/212,210
| PRIOR FILING DATE: 2000-10-17
| PRIOR FILING DATE: 2000-10-17
| PRIOR PILING DATE: 2001-03-16
| PRIOR PILING DATE: 2001-03-16
| PRIOR PILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-05-25
| NUMBER OF SEQ ID NOS: 3239
| SEQ ID NO 954
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                PRIOR APPLICATION NUMBER: 09/80,748
PRIOR FILING DATE: 2001-06-15
PRIOR PELLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
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ORGANISM: Homo mapiens
US-10-293-418-993
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CORGANISM: Homo sapiens
US-09-880-748-954
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

FRIOR APPLICATION NUMBER: 60/212,210

FRIOR APPLICATION NUMBER: 60/212,210

FRIOR APPLICATION NUMBER: 60/240,816

FRIOR APPLICATION NUMBER: 60/276,248

FRIOR APPLICATION NUMBER: 60/276,248

FRIOR APPLICATION NUMBER: 60/276,349

FRIOR APPLICATION NUMBER: 60/293,499

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 993

LENGTH: 250
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US-10-293-418-993
; Sequence 993. Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
PILE REFERENCE: PF523P2
; CURRENT PELICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR APPLICATION NUMBER: 60/340,817
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Conservative:
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DELETED1 (1-81) x US-10-898-408-12 (1-115)
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US-09-880-748-993
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Best Local Similarity:
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US-09-880-748-993
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Query Match: DB:

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US-10-308-817-83
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Publication No. US20030070185A1

GENERAL INFORMATION:
APPLICANT: GARGEOVITE, AVA

APPLICANT: KUCHERLAPATI, RAJU

APPLICANT: MIAPHOLZ, SUSAN

APPLICANT: MENDEZ, MICHAEL J.

APPLICANT: GREEN, LARRY

APPLICANT: GREEN, LARRY

TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN IG LOCI INCLUDING
                                                                                                                                                                                                                    Sequence 954, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFREENCE: PF5332
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT PILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-6-15
; PRIOR FILING DATE: 2001-6-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-31
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-01-17
; PRIOR FILING DATE: 2000-01-17
; PRIOR PRIOR DATE: 2000-01-17
; PRIOR PRIOR DATE: 2000-06-16
                                     1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG---
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DELETED1 (1-81) x US-09-880-748-954 (1-253)
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70 SerGlnAspThrSerAsn 75
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-293-418-954
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US-10-078-958-2
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TITLE OF INVENTION: PLURAL Wh AND WK REGIONS AND ANTIBODIES PRODUCED TITLE OF INVENTION: THEREFROM FILE REFERENCE: CELL 4.18 COM CURRENT APPLICATION NUMBER: US/10/078,958 CURRENT FILING DATE: 2002-02-19 PRIOR APPLICATION NUMBER: 08/759,620 PRIOR APPLICATION NUMBER: 08/759,620 NUMBER OF SEQ ID NOS: 79 SOFTWARE: Patentin Ver. 2.1 SEQ ID NOS: 79 SOFTWARE: Patentin Ver. 2.1
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Sequence 40, Application US/10194975

Publication No. US20030039649A1

GENERAL INFORMATION:

APPLICANT: Foote, Jefferson

TITLE OF INVENTION: Super Humanized Antibodies

FILE REFERENCE: 501231.01

CURRENT APPLICATION NUMBER: US/10/194,975

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 122

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PATENTIN VERSION 3.1
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CORGANISM: Homo sapiens
US-10-194-975-40
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69 ---IleSer 70
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ORGANISM: Homo sapiens
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RESULT 13
US-10-032-423A-87
US-10-032-423A-87
US-10-032-423A-87
Sequence 87, Application US/10032423A
Publication No. US20040002450A1
GENERAL INFORMATION:
THULE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/45
CURRENT APPLICATION NUMBER: US/10/032,423A
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOUTHWARE: FRASESQ for Windows Version 3.0
                                                      Sequence 87, Application US/10029988B
Publication No. US20040001839A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: WOISTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PRESEQ for Windows Version 3.0
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CORGANISM: Homo sapiens
US-10-029-988B-87
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69 ---IleSer 70
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US-10-032-423A-87
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LENGTH: 97
TYPE: PRT
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LENGTH: 97
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Publication No. US20040001822A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH BPITOPES, AND USES THEREOF
FILE REFREENCE: 10793/44
CURRENT APPLICATION NUMBER: US/10/032,037B
CURRENT PILING DATE: 2001-12-31
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
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Matches:
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Mismatches:
Sequence 83, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TILE REPERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE:
CURRENT FILING DATE:
SOFTWARE: PatentIn version 3.1
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SOFTHARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 97
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Best Local Similarity:
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ORGANISM: human
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US-10-032-037B-87
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Pred. No.:
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US-10-032-037B-87
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LENGTH: 97
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US-10-029-926B-87

US-10-029-926B-87

Sequence 87, Application US/10029926B

Publication No. US20040073011A1

GENERAL INFORMATION:

APPLICANT: HAGAY, et al.

TILLE OF INVENTION: SECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY

FILE REFERENCE: 107934/50

CURRENT APPLICATION NUMBER: US/10/029,926B

CURRENT APPLICATION NUMBER: 00/258,948

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR APPLICATION NUMBER: 60/258,948

NUMBER OF SEQ ID NOS: 203

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 87

TENNOTE: 07
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Matches:
Conservative:
Mismatches:
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US-10-453-689-83
; Sequence 83, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
    APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SEQ ID NOS 83
; SEQ ID NO 83
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69 ---IleSer 70
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ORGANISM: Homo sapiens
                            61 GATATTAGC 69
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69 ---IleSer 70
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; ORGANISM: human
US-10-453-698-83
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Db 50 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69

Db 69 ---IleSer 70

Search completed: August 4, 2005, 19:56:40

Job time: 107 secs
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Sequence:

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C;Species: Homo sapiens (man)
C;Dacession: 3-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 8:5606
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: 826800; MUID:92201299; PMID:11348029
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Matches:
Conservative:
Mismatches:
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   $44114
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   Percent Similarity:
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Query Match:
DB:
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A;Molecule type: DNA
A;Residues: 1-97 <WEN>
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-MODEL-frame+ n.D.p. model - DEV-X1p
-Q-/cgn2 1/USFTQ spool p/NOLAN463-3A/runat 04082005 120125 18808/app_query.fasta_1.263
-Q-/cgn2 1/USFTQ spool p/NOLAN463-3A/runat 04082005 120125 18808/app_query.fasta_1.263
-DB=PIR -QFMT=fastan - SUFFIX==pr - MAIRMATCH=0.1 -LOOPCL=0 - LOOPEXT=0
-UNITS=bits - START=1 - TRDE=1 - MATRIX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-OUTPMT=pto - NORM=SX - HEAPSIZE=500 - MINENEO - MAXLEN=2000000000
-UNFR-MINDIAN463-3A @CGN 1 1 63 @runat 0408205 120125 18808 - NCFU=6 - ICPU=3
-NO WMAP - LARGEQUERY - NEG SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG
-DEV TINEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPOFET=0.1 - YGAPOP=6
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1 GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC 81
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Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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Listing first 45 summaries
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S26898
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S47010
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G34964
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database

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Total number Minimum DB Maximum DB

Searched:

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C;Species: Homo sapiens (man)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837454
R;McInter (S:, Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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C;Species: Homo sapiens (man)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992,
A;Ftbe: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
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A;Actus: preliminary
A;Aclacule type: DNA
A;Residues: 1-97 <WEN>
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
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C;Reywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin
                     A; Molecule type: DNA
A; Residues: 1-97 < SANA
A; Residues: 1-97 < SANA
A; Cross-references: EMBL:X56364
A; Experimental source: V(H) 4.2
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
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A;Status: translation not shown
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S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Johns 1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V, Reference number: S26885; MUID:93021117; PMID:1404388
A;Recession: S26898
A;Accession: S26898
A;Residues: 1-97 <TOM>A;Residues: 1-97 <TOM <A;Residues: 1-999 <TOM <A;Residues: 1-999 <TOM <A;Residues: 1-999 <TOM <A;Residues: 1-97 <TOM <A;Residues: 1-999 <TOM <A;
                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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                        Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S78052; 823717
R;Harindranath, N.
R;Harindranath, N.
RyReference number: S78051
A;Reference number: S78052
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A;Reference number: $23716; MUID: 92031262; PMID: 1718404

A;Accession: $23717

A;Accession: $23717

A;Accession: $23717

A;Accession: $23717

A;Accession: $23717

A;Cross-references: BMBL: X54441

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>F;1-14/Domain: immunoglobulin homology <IMM>
F;29-111/Domain: immunoglobulin homology <IMM>
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Leu 122
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A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bir A;Reference number: 847010
A;Accession: 847010
A;Accession: S47010
A;Accession: S7010
A;Accession: A;Accessi
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Unn-1992 #sequence_revision 30-Unn-1992 #text_change 09-May-1997
C; Accession: PS0341
B; Ratech, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A; Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell A; Reference number: PS0341; MUID:92171937; PMID:1540170
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A; Residues: 1-133 < RAT>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 9-38/Region: framework 1
F; 39-43/Region: complementarity-determining 1
F; 34-77/Region: framework 2
F; 86-74/Region: framework 2
F; 56-74/Region: framework 3
F; 75-106/Region: framework 3
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C;Species: Homo sapiens (man)
C;Accession: JL0047
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J; Exp. Med. 167, 2011-2016, 1988
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
A;Accession: JL0047
A;Residues: 1-122 < BAE>
A;Residues: 1-122 < BAE>
A;Residues: L-122 < BAE>
A;Residues: L-122 < BAE>
A;Residues: L-102 < BAE>
A;Residues: I-102 < BAE>
A;Note: the authors translated the reading frame which extends to the stop codon; the set A;Note: this sequence belongs to the VH II subgroup
C;Superfamily: immunoglobulin nemology
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-105/Domain: immunoglobulin homology
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A;Reference number: S37453
A;Accession: S37454
A;Acture preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>A;Crose-references: EMBL>X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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R; Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
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---IleSer 78
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Ig heavy chain V region (DP-70 / 4.19) - human (fragment)
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92.40
74.07%
70.37%
66.00%
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88.40
70.37%
66.67%
63.14%
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S26905
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[1] Heavy chain V-IV region - human (fragment)

[2] Specias: Homo sapiens (man)

[3] C; Specias: Homo sapiens (man)

[4] Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

[5] Accession: B49028

[6] R; Timmers, B: Kenter, M: Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur Eur. J. Immunol. 21, 2355-2363, 1991

[7] A; Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphok A; Reference number: A49028

[7] A; Reterence number: A59028

[7] A; Reterence number: A59028

[7] A; Reterence number: A59028

[7] A; Residues: 1-143 < TIM

[7] A; Residues: 1-143 < TIM

[7] A; Residues: 1-143 < TIM

[7] A; Residues: B; Reterence extracted from NCBI backbone (NCBIN: 64473, NCBIP: 64472)

[7] Superfamily: immunoglobulin V region; immunoglobulin homology

[7] Superfamily: immunoglobulin homology < IMM>

[8] 15-97/Domain: immunoglobulin homology < IMM>
C; Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverme B.C.; Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Accession: A49
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92.40
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74.07$
70.37$
66.00$
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Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C,Accession: B23746
R,Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A,Title: Them 266, 2836-2842, 1991
A,Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiSanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4654-4664, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
C;Accession: G34964
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A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                     A;Wolecule type: protein
A;Reafdudes: 1-231 <LEO.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>
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Matches:
Conservative:
Mismatches:
Indels:
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Ig heavy chain V region - human (f.species: Homo sapiens (man) (7.5pecies: Homo sapiens (man) (man) (2.5pecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001 (2.5Accession: 544114 (man) (m
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                                                                  A;Cross-references: EMBL:231579; NID:g472968; PIDN:CAA83451.1; PID:g940525 CS:Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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60.71%
58.14%
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A; Status: preliminary
A; Molecule type: DNA
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of VA;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: EMBL:212370; NID:932960; PIDN:CAA78240.1; PID:g32961
A;Residues: 1-98 <TOM>A;Cross-references: EMBL:212370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
EMBO J. 8, 3741-3748, 1989
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Rederence number: S0
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514474
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: 514474
R;Van Bs, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H submitted to the EMBL Data Library, November 1990
A;Reference number: 514474
A;Reference number: 514474
A;Residues: 1970: DNA
A;Residues: 1-97 < csg.
A;Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology < IMM>
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TISSUE-Hodgkin lymphoma;
Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R., Hansmann M.L., Brauninger A.; Bubilted (MAY-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564425; CAD92032.1; -.
HSSP; P188232; IKCV.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
SMATY; SM00406; IGv; 1.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rearranged VH4-34 V gene segment (Fragment).
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061B05
HV46 MOUSE
08FWU0
08PFM2
TFC3 YEAST
Q96KX8
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Q926KS
YBXO, ARATH
YBXO, Q6HH60
Q6HH58
Q813F9
Q664Z3
Q8ZB26
HV61 MOUSE
Q8Z0Z7
Q6GMX1
HV60 MOUSE
Q6NYH3
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SEU ARATH
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-MODBL=frame+ n. 12p. model - DEV=Xlp
-DE-CONTOL = 1 0. 100 p. 100
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1612378 segs, 512079187 residues
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QBWUX4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                 DELETED1
                                                                                                                                                            August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0
66.0
66.0
66.0
61.7
60.3
58.1
58.1
56.0
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50.4
49.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922.4
44.29922.4
44.29922.4
44.39886.1
44.4
72.7
72.7
72.7
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69.3
69.1
                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                              OM nucleic
                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                            Run on:
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02
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Query Match:
DB:
                                                                                                                   QGGMX5
                                                                                    RESULT 3
                                                                                                     Q6GMX5
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                                                                                                                                                                                                                                                                                                                                             CTISSUB-Lymph,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Diatchenco, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenco, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., McKernan K.J., Malek J.A., Guaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahen J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

"Scherzation and initial analysis of more than 15,000 full-length human man and the state of the state
50 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, B019235, A4H19235.2;
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
Pfam; PF07654; C1-set; 4.
SMART; SM00409; IGG; 2.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595
119
64
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                     595 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
                                                                                                                                                                                       Created)
                                                                                                                                                     PRT;
                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.00292
92.40
74.07$
70.37$
66.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELETED1 (1-81) x Q8WUX4 (1-595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                                                     PRELIMINARY;
                                                                         ---IleSer 70
                                                   61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                     08WUX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
8
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A WEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J. Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McKwam P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
A Pahey J., Helton B.K. Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Nones S.J., Marra M.A.,
A Schmutz J., McKern Hannan J.E., Schmerch A., Schein J.E.,
A Jones S.J., Marra M.A.,
A Marra M.A., Smailus D.E., Schnerch A., Schein J.E.,
A Marra M.A.,
A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUBLEMENTS.

A Strausberg R.;
InterPro; IPR003599; Ig. 1.;
InterPro; IPR003599; Ig. 1.;
InterPro; IPR003509; Ig. 1.;
InterPro; IPR003506; Ig. 1.;
InterPro; IPR003506; Ig. 1.;
InterPro; IPR003596; Ig. 1.;
InterPro; IPR00406; IG; 1.;
INTERPRO; IRR INTERPRO; IG; 1.;
INTERPRO; IG; 1.;
INTERPRO; IG; 1.;
INTERPOSITE; PS50835; IG. IIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA; 65304 MW; 2A1E75F6AED85230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1197
                                                                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci. U.S.A. 99:16899-16903(2002).
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Mismatches:
Indels:
                                                                                                                                                                                                                                                  597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00292
92.40
74.07%
70.37%
66.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELETED1 (1-81) \times Q6GMXS (1-597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
69
                                                                                ---IleSer 96
GATATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60

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m

69

61 GATATTAGC

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=1., Grouse L.H., Dehmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.P., Juddin T.B., Toshiyuki S., Carninci P., Prange C.,
Altschards S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,
Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Altilaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Altilaton D.K., Muzny D.M., Schergren B.J., Lu X., Gibbs R.A.,
Altilaton D.K., Muzny D.M., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Altilaton D.K., Mark M.J., Schaltz J., Myers R.M., Butterfield Y.S.,
Altilaton D.K., Marra M.A.;
Altilaton D.K., Marr
                                 87
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 597 AA; 65274 MW; 2DĀFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597
19
1
                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                             597 AA
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nassr, folgon, nassr, n
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92.40
74.07%
70.37%
66.00%
                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGv; 1
                                                                                  61 GATATTAGC 69
                                                                                                                                    ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                            IGHM protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                 69
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                                                                                                                                                                                         RESULT
Q9BU10
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Riangner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schemfer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Buetow K.H., Schemfer C.P., Bhat N.K.,

Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Helton B.K. Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Strausberg R.;

Strausberg R.;

Strausberg R.;

Strausberg R.;

Strausberg R.;

REBL; BCG17355, AAH17356.2; -..

REBL; BCG17355, AAH17356.2; -..

RICEPPO; IPR003590, IG.

RICEPPO; IPR003597; IG.

RICEPPO; IPR003597; IG.

RICEPPO; IPR003597; IG.

RICEPPO; IPR003597; IG.

RICEPPO; IPR003596; IG.

RICEPPO; IPR003596; IG.

RICEPPO; IPR003596; IG.

RICEPPO; IPR003596; IG.

REBL; SW00409; IG.

REBL; SW00409; IG.

REBL; REBL; RESCORSS; IG.

REBL; REB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625
119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                      625 AA
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                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.00294
92.40
74.07%
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                                                                                                                                                                 PRELIMINARY;
---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                    IGHM protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similari
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01-DEC-2001 (
01-MAR-2004 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymph
88
                                                                                                                                                                                                         Q96AA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                          096AA6
                                                                                RESULT 5
Q96AA6
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DELETED1 (1-81) x Q96AA6 (1-625)

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Gaps:

DELETED1 (1-81) x Q9BU10 (1-597)

8 8

· 2

1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGGTCTCTCAAGAGTCGGGCGAGTCAG 60

GATATTAGC 69 ---IleSer 89

88

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RESULT 7
                                                                                                                                        06P4I8
                                                                  g
                                                                                                                                                                                   MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MI Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

MA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

M Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

M Diatchenko L., Warusina K., Parmer A.A., Rubin G.M., Hong L.,

M Diatchenko L., Warusina K., Parmer A.A., Rubin G.M., Hong L.,

M Schapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

M Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

M Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M Hilalon D.K., Muzny D.M., Sodergere B.J., Lu X., Gibbs R.A.,

M Hilalon D.K., Muzny D.M., Sodergere B.J., Lu X., Gibbs R.A.,

M Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

M Hitaleeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

M Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butrerfield Y.S.,

M Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M Generation and initial analysis of more than 15,000 full-length human
76 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94
                                                                                                                                                                                                                                                                                                                IGHM protein.
Homo saplens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                      597 AA
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                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01861; 1ADQ.
InterPro; IRR007110; Ig-like.
InterPro; IRR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC006180; AAH06180.1; -. HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELETED1 (1-81) x Q9BQB8 (1-597)
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                                                                     61 GATATTAGC 69
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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TISSUE=Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Riausherg R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haite F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninor P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mriting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Tand mouse cDNA sequences.",

R. Proc., Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                        Dolaco sapinia (menani).
Eukariota: Merazosa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (BE.2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC063384; AAH63384.1; -.

HSSP; PO1820; 1A7N.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR00359; Ig_C1.

InterPro; IPR00359; Ig_MHC.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR004059; Ig_MHC.

SMART; SM00407; Ig; 1.

SMART; SM00406; Ig; 1.

SMART; SM00406; IG; 1.

SMART; SM00406; IG; I.

SMART; SM00406; IG, IKE; 4.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS60836; IG_LIKE; 4.

SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576
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Mismatches:
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Matches:
                                                       05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last seq
05-JUL_2004 (TrEMBLrel. 27, Last anno
PRT;
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66.67%
PRELIMINARY;
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IISSUE=Primary B-Cells;
                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                          GHD protein.
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                                                                                                                                                                                          Name=IGHD;
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                             Q6P4I8;
Q6P4I8
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DELETED1 (1-81) x Q6P4I8 (1-576)

1 GANATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60 

69

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(1-81) x Q6GMX7 (1-477)
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                                                                                                                                                                                                                                                               TISSUE-Primary B-Cells,

TISSUE-Primary B-Cells,

ALESCHUIS-238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

AS Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

ALESCHUI S.F., Zeeberg B. M., Buetow K.H., Schaefer C.F., Bhar N.K.,

ALESCHUIS S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhar N.K.,

ALESCHUIS S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhar N.K.,

ADDITION M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

ADDITION M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

BOSAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

AN Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachey J., Helton B., Ketteman M., Madan A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rackeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein.
477 AA; 51631 MW; 9FES9C09C50CFF85 CRC64;
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2
2
1
                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                               477 AA
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Matches:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: BC073765; AA473765.11.
InterPro; IRR03599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003066; Ig. WHC.
InterPro; IPR003066; Ig. WHC.
Pfam; PF07654; Cl. seet; Z.
Pfam; PF07654; Ig. SMART; SM04009; IG; 4.
SMART; SM00407; IG; 1.
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39.22%
33.33%
58.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
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                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Primary B-Cells;
                                                   61 GATATTAGC 69
                                                                          ---ileser 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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Pred. No.:
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                         11
                                                                          96
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DB:
                                                                                                                               Q6GMX7
                                                                                                   RESULT 8
Q6GMX7
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90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109
                                            70 IleSerHisSerGlySerThrThrTyrAsnProSerLeuLysSerArgValThrLeuSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
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4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAGGAT 63
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1-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-II region ARH-77 precursor.
17 heavy palens (Human).
18 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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D segment.
J segment.
By similarity.
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Matches:
Conservative:
Mismatches:
Indels:
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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78.40
66.67$
62.96$
56.00$
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146
115
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                                                                                                                                                                   64 ATT-----
                                                                                                                                                                                                                                                                                                                                            ------- 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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SEQUENCE
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DB:
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Strausberg R.;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThr 122
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                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Full-length cDNA clone CSODLO04YM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=mix FVB/N; TISSUE=Mammary tumor; MBDLINE=2388257; PubMed=1247992; DOI=10.1073/pnas.242603899; Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.; Klausner R.D.; Collins F.S.; Wagner L., Shenmen C.M.; Schuler G.D.; Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.; Hopkins R.F.; Jordan H., Moore T., Max S.I.; Wang J.; Hsieh F.; Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M., Hong L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGT---
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                     TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX248300; CAD62627.1; -. HSSP; PO1820; 1G7J. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7D1E2302410E4F8C CRC64;
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33
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Matches:
Conservative:
Mismatches:
Indels:
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  139 AA
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  PRT;
                                                                                                                           Homo sapiens (human) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 139 AA; 15573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.-
PROSITE; PS50835; IG_LIKE; 1.
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73.70
35.71
30.36
52.64
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PRELIMINARY;
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                           TISSUE=B cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
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                   286SX2;
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90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrThrGluAspThr 109
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko Y., Souffard G.G. Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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TISSUB-Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AMN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
HSSP; D1820; IG7J.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF07644; C1-set; Z.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 protein.
479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AlaThrTyrTyrCysAlaSerArgGlyTyr----SerTrp 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Conservative:
Mismatches:
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Gaps:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELETED1 (1-81) x Q99M22 (1-479)
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72.60
33.93%
30.36%
51.86%
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Best Local Similarity:
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DELETED1 (1-81) x Q96EY0 (1-620)
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Carimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Jones S.J., Marza M.J.,
Jones S.J., Marza M.J.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAGGATATTAGCAGC 72
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -
INCEPTO; IPR001559; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_V.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
InterPro; IPR0054; Ig_V.
InterPro; IPR0040596; Ig_V.
InterPro; IPR004059; Ig_V.
InterPro; IPR00407; Ig; 4.
SWART; SW00407; IgG1; 3.
SWART; SW00407; IGG1; 3.
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465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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113
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Last annotation update)
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Mismatches:
Indels:
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Matches:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELETED1 (1-81) x Q6GMX6 (1-465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
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72.00
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51.43%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Primary B-Cells;
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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01 026EY
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AC 096EY
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DT 01-DE
DT 01-DE
DT 01-DE
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                RAHARAH KARAHAN KARAHA
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Wilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Maray D.W., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raciquez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strauberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, BC011857, A4H11857.2; ...

PIR, $15590; $15590.

R HSSP; POL020; 1G70.

R InterPro; IPR001359; IG.

R InterPro; IPR001359; Ig.

R InterPro; IPR001359; Ig.

R InterPro; IPR00356; Ig.

R InterPro; IPR00356; Ig.

R SMART; SM00409; IG.1.

R SMART; SM00406; IG.1.
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113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.95 · 72.00 80.00% 65.00% 51.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.
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TISSUE=Primary B-Cells;
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse
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Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
"Targeting human immunodeficiency virus type 1 reverse transcriptase
by intracellular expression of single-chain variable fragments to
inhibit early stages of the viral life cycle.";
J. Virol. 70:3392-3400(1996).
EMBL; U48716; AAB64342.1; 25-OCT\_2004 (TrEMBLrel. 28, Created)
25-OCT\_2004 (TrEMBLrel. 28, Last sequence update)
25-OCT\_2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
Anti-HIV-1 reverse (Tremscriptase single-chain variable.
Eukaryota: Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae 262 AA. TISSUE=Hybridoma; MEDLINE=96211469; PubMed=8648670; PRELIMINARY; SEQUENCE FROM N.A. NCBI\_TaxID=10090; Q65Z11

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
Homo sepiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[11]
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Clin. Immunol Immunopathol. 87:184-192(1998).
EMBL; AF035041; AAD56277.1; -.
PIR; PH0876; PH0876.
PIR; PH0876; PH0876.
PIR; P1879; P01820; 1G7J.
InterPro: IPR007110; Ig-like.
InterPro: IPR007110; Ig-like.
InterPro: IPR007110; Ig-like.
SMART; SM00406; IGV.
SMART; SM00406; IGV.
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.-c.
InterPro; IPR003596; Ig.-c.
InterPro; IPR00409; Ig.-c.
SNART; SN00409; IG.2.
SNART; SN00409; IG.2.
SNART; SN00408; IG.2.
RNART; SN00408; IG.2.
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MEDDINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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DELETED1 (1-81) x Q9UL73 (1-119)

Search completed: August 4, 2005, 19:37:58 Job time : 113 secs

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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulatic; immunosuppressive; immunostimulatic; antilAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 VEGF anti
Antibody
Antibody
VH gene 1
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Strepativ
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CAMBRIDGE ANTIBODY TECHNOLOGY
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16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2001; 2001WO-US019110.
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                                       WO200202641-A1.
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ABP45322;
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(CAMB-)
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 Command line parameters:
-MODEL=frame+ n2p.model - DEV=Xlp
-0=/CORD_1/USPTO spool_p/NOLAN463-18P/runat_04082005_120453_19604/app_query.fasta_1.263
-0=/CORD_2_1/USPTO spool_p/NOLAN463-18P/runat_04082005_120453_19604/app_query.fasta_1.263
-0B-A_Geneseq -OFMT=fastan -SUFPIX=x=g -MINMATCH=0.1 -LOOPGL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=100 -TRANS=human40.cdi -LIST=45
-OTFPT=ptc -NORM=ext -HRAFSIZE=560 -MINLEN0 -MAXLEN=200000000
-USER=NOLAN463-3B @CGN 1 1 224 @runat_04082005 120453_19604 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBECCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -PGAPOP=6
-PGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELDP=6 -DELEXT=0.1
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Adg96149 Single ch
Ada89274 Human ant
Aaw62794 Amino aci
Aay05694 Multiple
Abg78212 Human Fv
Abg91903 Human ant
Abc27107 Human ger
Adb75646 Human pro
Add28104 Lymphoma
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1 CGGGCGAGTCAGGATATTAG......ACAACCCGTCTCTCAAGAGT 81
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       version 5.1.6
- 2005 Compugen Ltd.
                                                 protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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RESULT 3
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                                                                                                               This invention describes novel antibodies that immunospecifically bind to
                                                                                                                       Blymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                             acquired immunodeficiency syndrome (AIDS)). ABP41990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                               Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody that immunospecifically binds BLyS SeqID 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; Bcall proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis, asthma: rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                     diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
Vaughan T, Hilbert
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sSer 65
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This invention relates to novel antibodies that immunospecifically bind
to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
chromosome 1343 and encodes a protein that is a member of the tumour
chromosome 1343 and encodes a protein that is a member of the tumour
necrosis factor superfamily and induces both in vivo and in vitro B cell
proliferation and differentiation. Specifically, it refers to single
chain antibody molecules (scYPs) derived, preferably, from the variable
the neavy CDR3 region that immunospecifically bind to a polypeptide.
Cf fragment thereof, of either human, murine, rat or monkey BLyS. The
fragment invention refers to the use of such antibodies in various methods
for the detection, diagnosis and prognosis of diseases related to the
aberrant expression or inappropriate function of BLyS or its receptor. As
such, these compositions are useful for identifying immune disorders
including mysathenia gravis and multiple sclerosis, inflammatory
disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
as AIDS and proliferative disorders including leukaemia, carcinoma and
lymphoma. Accordingly, they can be described as exhibiting various
activities such as antirheumatic, antiallergic and cytostatic. This
colypeptide sequence is a single chain antibody that binds BLyS of the
invention. NOTE: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format
cthe printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                          Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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                                                                  16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
14-NOV-2002; 2002WO-US036496.
                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                           Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                              WPI; 2003-505530/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 253 AA;
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DB:
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The present invention describes a protein comprising an immunoglobulin (1g) heavy chain variable (VH) domain and an Ig light chain variable (VL) domain. The protein blinds a complex comprising a major histocompatibility complex (MHC) and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide in the absence of the MHC. The peptide is a peptide fragment of gp100, MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition comprising the novel protein and a carrier; (2) a cytotoxic T cell comprising one or more nucleic acids for expressing the Ig that binds a complex having an MHC and a peptide, does not substantially bind the comprising one or more nucleic acids for expressing the Ig that binds a comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the competion of the MHC. Peptide complex, (7) expressing an antigen-binding protein; (8) ablating or killing a target cell that a comprise a sequence that encode the protein; (6) identifying the protein a subject, and (10) detecting an MHC-peptide complex in a sample. A protein of the invention has cytostatic activity, and can be used in gene therapy. The protein in a unstand or preventing a composition for treating or preventing a peptide complex where the peptide component in as peptide on an MHC. Peptide complex on an entrance of the protein in a subject, and the protein in a serior of an antiponent in a septide complex on an entrance of the protein of an antiponent in a septide complex of a peptide complex of a peptide on an entrance of the protein in a septide complex of a pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
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                   immunoglobulin; Ig; heavy chain variable domain;
light chain variable domain; major histocompatibility complex; MHC;
gpl00; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
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(TECR ) TECHNION RES & DEV FOUND LTD.
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99.90
50.00$
47.83$
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                                                                                                                                                                                                         WO2003070752-A2.
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                                                                                                                                                              Homo sapiens.
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                                                                                                                                      Synthetic
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                                                                                             cancer.
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transgenic Xenomice, created using the method of the invention. The specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin (Ig) locus, so that the mammal does not display normal B-cell development. The modifications that comprise an inactivated human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in miner configuration, the human bay chain Ig locus comprising a human constant region and regulatory and switch sequences, human J-H genes, and human V-H genes and an inserted human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, inserted are chain Ig locus comprising a human kappa constant region, J-kappa genes, and human B-cell development in the human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, and human kappa constant region, J-kappa genes, and v-kappa genes inserted are cand v-kappa genes inserted are selected to restore normal B-cell development in the mammal. The cransgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e-g. when exposed to human IL-8, EGFR or TNF- alpha respectively
                                                                                                                                                                                                                                                                                                               Human; immunoglobulin; Ig; transgenic; non-human mammal; inactivated endogenous Ig locus; B-cell development; Muman heavy Chain Ig locus; micro constant region; J-H; D-H; V-H gene; kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa; production; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New transgenic non-human mammals - having an inactivated immunoglobulin locus and a near complete human immunoglobulin locus, used for production of human antibodies.
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Mendez M,
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                                                                                                                                                                                                                                                                                   Amino acid sequence of a human antibody fragment.
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Mismatches:
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Matches:
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                                                                                                                                                                            AAW62794 standard; peptide; 80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kucherlapati R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US023091
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98.20
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                                                                                                      64 rLeuLysSer
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-1996;
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25 GlyLys----GlyLeu----GluTrplleGlyGlulleAsnHisSerGlySerThrAsnT 42
                                           Multiple sclerosis patient CSF B-cell VH region (clone 4d76)
                                                                                                                                                                                               Multiple sclerosis; cerebrospinal fluid; CSF; B-cell; heavy chain variable region; VH gene; somatic hypermutation; B-cell clonality; RA gene; diagnosis; human.
80
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                                                                                                                                                                                                                                                                                                      note= "replaces Glu of RA"
                                                                                                                                                                                                                                                                                                                                       note= "replaces Gly of RA"
                                                                                                                                                                                                                                                                                                                                                        note= "replaces Phe of RA"
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                                                                                                                                                                                                                                                                                                                                                                                                           Gly of RA"
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Indels:
Gaps:
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                                                                                                                              AAY05694 standard; protein; 97 AA
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                                                                            62 ACAACCCGTCTCTCAAGAGT 81
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/label= CDR1
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|abel= CDR2
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/label= FR2
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/label= FR1
                          DELETED2 (1-81) x AAW62794 (1-80)
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/label= FR3
                                                                                                                                                                (first entry)
70.14%
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Query Match:
DB:
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fund (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF sequences of Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a heavy chain variable region (VH) as predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of B-cell clonality by amplification or enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Fv molecule hypervariable region related peptide #87.
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Matches:
Conservative:
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Indels:
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97CA-02216595.
97CA-02220245.
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                                                                                                                                                               WPI; 1999-276985/23.
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  19-SEP-1997;
04-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                     The invention relates to a peptide or polypeptide comprising an FV molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and FV is a single chain FV (scFV) or a disulfide FV (dsFV). The peptide, optionally in association with or attached, compined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human FV molecule hypervariable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                     Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levanon A;
                                                           Guy R, Lipschitz O, Szanton E,
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                  Claim 13; Page 193; 232pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   related peptide of the invention
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                                   (BIOT-) BIO-TECHNOLOGY GEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG91903 standard; protein; 97
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65.62%
59.38%
70.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                          Lazarovits J,
Peretz T;
                                                                                              WPI; 2002-619166/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97 AA
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Pred. No.:
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                                                          Hagai Y, L
Plaksin D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG91903;
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DB:
                                                                                                                                                           cells.
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ABG91903
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infortant in physiclogical phenomena such as cell rolling, metaetasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment for its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune capacitopes are useful for inhibiting cell rolling, inflammation, autoimmune the chief are epitopes are useful for inhibiting cell rolling, inflammation, autoimmune capacitopes are useful for inhibiting cell rolling, inflammation, autoimmune complexed in a patient, cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells, in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-contein interactions. This sequence represents a human antibody fragment of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated epitope present on cancer cells and
                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GlyLys----GlyLeu----GluTrp11eGlyGlu11eAsnHisSerGlySerThrAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mar-Haim
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Peretz T,
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Matches:
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Mismatches:
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Kooperman L,
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                                                                                                                                                                                          (BIOT-) BIO-TECHNOLOGY GEN CORP
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                                                 31-DEC-2001; 2001WO-US04942
                                                                                                        29-DEC-2000; 2000US-00751181.
29-DEC-2000; 2000US-0258948P.
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Richter T,
                                                                                                                                                                                                                                                                                                                                  WPI; 2002-674776/72.
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Query Match:
DB:
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11-JUL-2002.
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antibody library, CD1 region, CD2 region; VH region, VL region; immunoglobulin; CD3 region; TM1 scFv; human.

Human protein relating to the invention SEQ ID NO:55

04-DEC-2003 (first entry)

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The inversion describes a meribod of mananistic antibody.

Comprising making chimmeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a humanisation and converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support on human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparison framework sequences between non-human and human antibodies. This sequence represents a human heady chain variable region gene segment used in the
                                                                                                                                                                                                                                                                                                                                                                                                  Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of making a humanised antibody
Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 31pp; English
                                                                                                                                                                                                  12-JUL-2002; 2002US-00194975
                                                                                                                                                                                                                                           12-JUL-2001; 2001US-0305111P.
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Best Local Similari
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                                                                                  Homo sapiens
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and

Highly stable artificial antibody libraries with super-repertory little contamination from unexpressible ones, useful as tool in proteomics and e.g. for diagnosis and treating various diseases.

Okui

Takayanagi A,

Shimizu N,

(UYKE-) UNIV KEIO.

WPI; 2003-449818/42.

22-NOV-2002; 2002WO-JP012236. 22-NOV-2001; 2001JP-00358602

WO2003044198-A1

30-MAY-2003

Homo sapiens

Disclosure; Page 101; 108pp; Japanese.

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The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CD1 and CD2 regions of immunosplobulin gene and a fragment containing the CD3 region by PCR, respectively, producing VH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B-cell; malignant; immunoglobulin; immunoglobulin variable region;
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ADB75646 standard; protein; 97 AA

ADB75646

ADB75646;

81 65

DELETED2 (1-81) x ABO27107 (1-97)

42 62 5

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ACAACCCGTCTCTCAAGAGT

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Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
              VEGF antibody heavy chain variable region VH_4-34
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                                                                                                  WO2003074679-A2.
                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (l) treating a patient suffering from or at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor inhibiting glycosylation of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (s) has cycostation the surface of Ig of lymphoma cells. (s) has glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the cycosylation of the present invention.
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant
Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma.
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                                                                                  WO2003074059-A2.
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                                                Synthetic.
Homo sapiens.
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                                                                                                            12-SEP-2003
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody especially the stability, or antigen blinding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody may be variable region sequence used to illustrate the invention.
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variable
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Matches:
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                                                                                                                          Marshall SA,
                                                                                                                                                                                                                                                                                                                          Example 6; Fig 16a; 135pp; English
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01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
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                                                                                                                          Lazar GA, Desjarlais JR,
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                                                                                                                                                                        WPI; 2003-722066/68.
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                                                                          (XENC-) XENCOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                               positions.
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ID ADF1
XX AC ADF1
XX DT 12-F
XX DE ANE
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variable region; human.
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IID ADJ8

XX AC ADJ8

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DT 06-W

DX VH 9

XX HOMC
   %XCCCCCCCCCCX%X444X4X4X4X4X4X4X6XAX6XX8XX8XX8XX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                       physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position (s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                      Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
Antibody, stability, solubility, antigen binding affinity, variable region; human.
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Matches:
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                                                                                                                                                                                                                                                                     Desjarlais JR, Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                                               Example 16; Fig 40a; 135pp; English
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29-MAY-2002; 2002US-0384197P.
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Query Match:
DB:
                                                                                          WO2003074679-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97 AA;
                                                                                                                                                                                                                                     (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                               Homo sapiens.
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least noe antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical property of an antibody, especially the stability, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody way be variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybrid antibody; antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dahiyat
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                                                                                                                                                                                                                                                                                                                                       Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 2a; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ80323 standard; protein; 97 AA.
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29-MAY-2002; 2002US-0384197P.
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                                                 WO2003074679-A2
                                                                                                                                                                                                                                                                                      (XENC-) XENCOR,
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Homo sapiens
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AAB01949;

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable cregion of the initial antibody; (iii) selecting a first component of the sequence of the first component to sequence contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (ii) comparing the sequence of the than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (iii) comparing the sequence of the second component to sequence contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (viii) selecting a sequence from the database of antibody to the sequences from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the component component complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody the method is useful for producing a hybrid method of the method is useful for producing a manibody fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 83; 77pp; English
                                                                                                                                                                                                                  03-DEC-2002; 2002WO-US038450
                                                                                                                                                                                                                                                                                                                              03-DEC-2001; 2001US-0336591P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-513753/48.
WO2003048321-A2
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                                                                                                      12-JUN-2003.
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97 17 0 8 8 9 9 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: DELETED2 (1-81) x ADJ80323 (1-97) 98.20 65.62% 59.38% 70.14% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: 

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61
  59
42
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a ò RESULT 15 AAB01949 ID AAB0 XX

AAB01949 standard, protein; 114 AA

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Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M; IgM; V gene diversity; directed constitutive hypermutation; tearget sequence diversification; terminal deoxymucleotidy1 transferas TdT; clonal expansion; selection; heavy chain variable region; VH;
                           Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N.
                                                                                                                      /note= "Encoded by CAG"
                                                                                                                                                                                                                         Sale JE, Neuberger MS, Cumbers SJ;
                                                                                                       Location/Qualifiers
                                                                                                                                                                              98GB-00022104.
99GB-00001141.
99GB-00013435.
                                                                                                                                                                 99WO-GB003358
                                                                                                                                                                                                           (MEDI-) MEDICAL RES COUNCIL.
             18-SEP-2000 (first entry)
                                                                                                                                                                                                                                       2000-317971/27.
                                                                                                               Misc-difference 71
                                                                                                                                                                                                                                             N-PSDB; AAA52435
                                                                      mutant; mutein
                                                                                                                                    WO200022111-A1
                                                                                                                                                                              09-OCT-1998;
19-JAN-1999;
09-JUN-1999;
                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                 08-OCT-1999;
                                                                                                                                                  20-APR-2000
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Lymphoid cell line preparation useful for producing gene products having desired activity, involves screening and selecting cells having ongoing target sequence diversification and higher mutation rates.

Example 5; Page; 69pp; English.

The invention relates to a method of preparing a lymphoid cell line capable of directed constitutive hypermutation of a target capable of directed constitutive hypermutation of a target nucleic acid mutation exceeds that of other nucleic acid mutation for cate of target nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid encoding the target gene operably linked to a sequence which directs hypermutation e.g., terminal deoxynucleotidyl transferase (TdT), in the lymphoid cell line, and identifying a cell or cells which express a mutated gene product with the desired activity. One or more clonal populations of the identified cells is established, and cells with an improved activity of interest are selected. These steps may be iteratively repeated until a gene product with a desired of the invention are used for directed constitutive hypermutation of a nucleic acid region in the preparation of a gene product, preferably an enzyme or an immunoglobulin (Ig) with a desired activity. In the exemplifications of the invention, IgM-secreting Ramos cells were selected for use as they undergo hypermutation of an acid region (WH). Sequences AAB01949-B01954 represent various mutant Ramos cell IgM WHS (AAB01949-B01954) which have lost the ability to bind anti-idlotype antibodies (anti-idl Ab) relative to the wild-type VH (AAB01949). Note: The present sequence is not shown in the specification, but is derived to the wild-type vH (AB01949).

Sequence 114 AA;

Alignment Scores: Pred. No.:

Length:

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Matches:	Conservative:	Mismatches:	Indels:	Gaps:
98.20	65.62%	59.38%	70.148	Э
Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

DELETED2 (1-81) x AAB01949 (1-114)

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Search completed: August 4, 2005, 20:00:48 Job time: 123 secs

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Sequence 169, Applacemence 2, Applia Sequence 7, Applia Sequence 7, Applia Sequence 7, Applia Sequence 39, Applia Sequence 65, Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 13, Appl
Sequence 837, Appl
Sequence 79, Appl
Sequence 17, Appl
Sequence 16, Appl
Sequence 16, Appl
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Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: HOMJO, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
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US-08-466-163B-5

US-09-802-096-5

US-09-802-096-5

US-09-372-425A-2

US-09-471-276-837

US-09-471-276-837

US-08-138-197-16

US-09-138-197-16

US-09-138-197-16

US-09-726-1197-16

US-09-726-119A-169

US-09-726-119A-169

US-09-726-119A-169

US-09-726-119A-169

US-09-726-119A-169

US-09-726-119A-169

US-09-726-119A-169

US-09-726-119A-169

US-09-90-070-776-198-199

US-09-490-070-65

US-09-490-153-39

US-09-490-153-65

US-09-490-153-75

US-08-630-820-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: US
ZIF: 0110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INPORMATION: NAME: Freeman, John W. REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELLEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-545-809A-140
US-08-851-362D-22
                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
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COUNTRY:
    RESULT 1
      Command line parameters:
-MODEL=frame+ n2p.model - DEV=Xlp
-MODEL=frame+ n2p.model - DEV=Xlp
-Q=/Con2_1/USFPTO_gopol_p/NOLAN463-13B/runat_04082005_120454_19634/app_query.fasta_1.263
-Q=/Con2_1/USFPTO_gopol_p/NOLAN463-13B/runat_04082005_120454_19634/app_query.fasta_1.263
-DB=1ssued_Patents AA -QFWT=fastan - SUFFTX=rai - MINWATCH=0.1 -LOOPCL=0
-LIST=AE5 - DOCALIGN=2.00 - THR SCORE=POT - THR MINED - ALIGN=15
-MODBELGCAL - OUTFMT=PLO - NORM=ext - HEAPESIZE=500 - MINLEN=0 - MAXIEN=20000000
-USER=NOLAN463-3B @CGN 1 1 46 @runat_04082005_120454_19634 - NCFU=6 - ICPU=3
-NO_MMAP - LARGEQUERY - NGG GCORES=0 - WAIT - DSPBELCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.1 - FGAPOP=6
-FGAPEXT=0.1 - YGAPOP=10 - YGAPEXT=0.1 - DELDEXT=0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118, App
Sequence 4, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7, App
5, App
Appli
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6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl
                                                                                                                                                   4, 2005, 19:53:13 ; Search time 29.5 Seconds (without alignments) 409.937 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                    CGGCCGAGTCAGGATATTAG......ACAACCCGTCTCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued Patents AA:*
1: /cgn2_6/ptOdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptOdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptOdata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptOdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptOdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptOdata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-08-793-450-4
US-09-203-768A-2
US-09-372-425A-6
US-09-372-425A-6
US-09-490-070A-25
US-09-490-153-25
US-09-490-153-25
US-09-491-374-25
US-08-545-809A-137
US-08-545-809A-137
US-08-545-805-137
US-08-545-815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                          DELETED2
                                                                                                                                                          August
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Match
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70.1
70.1
70.1
70.1
66.6
65.8
65.8
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65.8
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                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
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Database

12243321

Result

Total number Minimum DB Maximum DB

Searched:

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Alignment Scores:
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Sequence 4, Application US/08793450

Sequence 4, Application US/08793450

Sequence 4, Application US/08793450

Sequence 4, Application

GENERAL INFORMATION:

APPLICANT: BEDELAW. LENA

APPLICANT: CACACREK, MICHEL

APPLICANT: CACACREK, MICHEL

APPLICANT: CHABRITICH:

MONGEN OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: PACOUTY: USA

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STRATE: USA

CONTRY: USA

CONTRY: USA

CONTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Benefilm Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,450

FLING DATE: 03-MAR-1997

CLASSIFICATION NUMBER: E4,618

REGISTRATION NUMBER: E4,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 660-118-0 PCT

TELEPAN: NAME: OBLON, NUMBER: 660-118-0 PCT

TELEPAN: TELEPAN: TO 3-413-3000

INFORMATION FOR PST TO NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO. 1. NO.
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119
22
33
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELETED2 (1-81) x US-08-545-809A-118 (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 yrAsnProSerLeuLysSer 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                4.16e-05
98.20
65.62%
59.38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                         LENGTH: 116 amino acids TYPE: amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-793-450-4
                                                                                                         // TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-545-809A-118
                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-793-450-4
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Sequence 2, Application US/09203768A
Sequence 2, Application US/09203768A
Sequence 2, Application US/09203768A
Sequence 2, Application US/09203768A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
TITLE REFERENCE: PIX 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 139
WANDE. NOW
                                                                                                                                                 Sequence 8, Application US/08793450
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
APPLICANT: EDELMANITE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHMAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
22
3
3
0
      123
2 2 8 3 0 0 0
     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                       DELETED2 (1-81) x US-08-793-450-4 (1-123)
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                                                                                                                                                                                                                                        4.25e-05
98.20
65.62
59.38
70.14$
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98.20
65.62%
59.38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-203-768A-2
                                Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                      US-09-203-768A-2
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US-08-793-450-8
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DB:
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Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                        US-09-372-425A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09372425A;
Sequence 6, Application US/09372425A;
Patent No. 6475749;
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly Lip
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELETED2 (1-81) x US-08-793-450-8 (1-472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ACAACCCGTCTCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.20
65.62%
59.38%
70.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               JECUMPACE: 703-413-2220
TELEPHONE: 703-413-2220
TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-793-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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Pred. No.:
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US-09-372-425A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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SOFTWARE: Petentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILLING DATE: 18-A06-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Veter
APPLICANT: Go, Liming
APPLICANT: Go, Liming
APPLICANT: Moroney, Sinon
APPLICANT: Moroney, Sinon
APPLICANT: Moroney, Sinon
APPLICANT: Plueckthun, Andreas
ITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
         ATTORNEY JOHE:
NAME: Oldenakmp, David J.
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELEPHONE: (310) 788-5000
TELEPHONE: (310) 788-5100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELETED2 (1-81) x US-09-372-425A-6 (1-429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MS-025-769B-25
1) Sequence 25, Application US/09025769B
2: Patent No. 6300064
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 93.20
65.62$
56.25$
66.57$
                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity:
FILING DATE:
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SEQUENCE CHARACTERISTICS:

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24
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVATION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
                                                                                                                                                                                                                                                                                                                                                                            DELETED2 (1-81) x US-09-025-769B-25 (1-118)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ 1D NO: 25:
; TELEFAX: (212)596-9000
TELEFAX: (212)596-9090
: INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acids
STRANDEDNESS:
TOPOLOGY
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                                                                                                                                                                                                                                            0.000291
92.10
50.00%
47.73%
65.79%
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MOLECULE TYPE: protein
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Best Local Similarity: (Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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50.00$
47.73$
65.79$
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STATE: New York
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ZIP: 10021
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Best Local Similarity:
Query Match:
DB:
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US-08-545-809A-137
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TGGTTAGCCGAAATCATAGTGGAAGCACCAACTACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; Patent No. 100284210N:
; APPLICANT: Knappik, Achim
Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; Pack, Peter
; TITLE OF INTENTION: Protein/(Poly) peptide libraries
; NUMBER OF SEQUENCES: 373
                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: James F. Haley, Jr., Esg.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
                                                                                                                                                                                                                                                                                           Gaps:
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TELEPHONE: (1215)596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 118 amino acids
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                                                                                                                                                                                    0.000291
92.10
50.00%
47.73%
65.79%
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STATE: New York
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                       25 -----TGGTTAGCCGAAATCAATCATGGGAAGCACCAACTACAACCGTCTCTCAA 77
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Honjo, Tasuku
APPLICANT: Mateuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Freeman, John W.
TYPE: amino acid

STRANDEDNESS: «Unknown»

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06501/004001
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                                                                                                                                                                                                                                                                              DELETED2 (1-81) x US-09-490-324-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 137, Application US/08545809A; Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELERX: 200154
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                              0.000291
92.10
50.00%
47.73%
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Best Local Similarity:
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64 8Ser 65
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US-08-545-809A-137
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DB:
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                                                                                                                                                                                                                                                                                                   sequence 835, Application US/09471276

patent No. 6822072

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERRNCE: GENEST. 025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT PILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622

SOFTWARE: Patent.pm
SEQ ID NO 8355

LENGTH: 147
                                                                                                                                             69 GlyLys----GlyLeu----GluTrp1leSerGluIleAspHisGlyGlyAsnThrAsnT 86
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116
33
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         Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Indels:
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US-08-466-151-5
; Sequence 5, Application US/08466151
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65.62%
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52.27%
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                                   Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                                    GAGT 81
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US-09-471-276-835
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Alignment Scores:
Pred. No.:
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33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
              APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
CORRESPONDENCE: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELETED2 (1-81) x US-08-466-151-5 (1-130)
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
RICH APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION NUMBER: 07/87495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/87495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/87495
FILING DATE: 14-AUG-1991
ATTORNEY/GRENT INFORMATION:
                                                                                                              ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA ZIP: 94080
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Amino Acid
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Best Local Similarity:
GENERAL INFORMATION:
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21 32

RESULT 13

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WE-DOLD TO TO THE MACRO TO THE MEDICAL TO WE ADDITION OF SEQUENCE 5, Application US/09802077;
Patent No. 6699472;
Patent No. 6699472;
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Peneta, Leonard G.
TILE REFERENCE: D0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT PAPLICATION NUMBER: US 08/465,617
PRIOR APPLICATION NUMBER: US 08/465,617
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR PLING DATE: 1995-01-26
PRIOR PLING DATE: 1992-06-14
PRIOR PLING DATE: 1992-05-07
PRIOR PLING DATE: 1992-06-07
PRIOR PLING DATE: 1991-08-14
PRIOR PLING DATE: 1991-08-14
PRIOR PLING DATE: 1991-08-14
PRIOR PLING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Indels:
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Pred. No.:
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; Sequence 5, Application US/09802096
; Ratent No. 668539
; GENERAL INFORMATION:
    APPLICANT: Dardieu, Paula M.
; APPLICANT: Presta, Leonard G.
    TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended FILE OF INVENTION NUMBER: US/09/802,096
; TITLE OF INVENTION NUMBER: US 08/09/802,096
; FILE REPREMENT: 1992-03-15
; PRIOR FILING DATE: 1992-03-15
; PRIOR FILING DATE: 1992-03-15
; PRIOR PILING DATE: 1992-08-14
; PRIOR FILING DATE: 1992-08-14
; PRIOR FILING DATE: 1992-05-07/744,768
; PRIOR FILING DATE: 1992-05-07
; PRIOR FILING DATE: 1991-08-14
; RUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Matches:
Conservative:
Mismatches:
         Sequence 5, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/7744,768
PRIOR APPLICATION NUMBER: US 07/7744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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ORGANISM: Mus musculus
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Best Local Similarity:
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Pred. No.:
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US-08-466-163B-5
US-08-466-163B-5
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Search completed: August 4, 2005, 20:06:46 Job time : 31.5 secs

Title: Perfect score: Sequence:

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Scoring table:

Minimum DB seq Maximum DB seq

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Sequence 128, App
Sequence 12, Appl
Sequence 44315, A
Sequence 90, Appl
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PF23.

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21
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. Sequence 1333, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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Match Length DB
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-MODEL=frame+ n2p.model - DEV=Xlp
-MODEL=frame+ n2p.model - DEV=Xlp
-G=/CG012 1/USFPTO spool p/NOLAN463-3B/runat_04082005_120456_19700/app_query.fasta_1.263
-G=/CG02 1/USFPTO spool p/NOLAN463-3B/runat_04082005_120456_19700/app_query.fasta_1.263
-DB=Published Applications AA -OFMT=fastan -SUFFIX=Tapb -MINNATCH=0.1
-LOOPCL=0 -LOÖPEXT=0 -UNTTS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 - DOCALIGN=200 -THR SCORE=PDC - THR MAX=E00
-AALIGN=15 -MODE=LOCAL -OUTFMT=pct - NORM=ext - HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=NOLAN463-3B_@CGN_1_1 199_@runat_04082005_120456_19700
-NCPU-S - ICCUPA - NOARP -LARGEQUERY - NEG SCORESS=0 - MANT - DESBLOKE=100
-LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.1
-FGAPOP=6 - FGAPEXT=0.1 - YGAPOP=10 - YGAPEXT=0.1 - DELOP=6 - DELEXT=0.1
                                                                                                                                                 August 4, 2005, 20:04:58; Search time 105.5 Seconds (without alignments) 599.473 Million cell updates/sec
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1 CGGGCGAGTCAGGATATAG.....ACAACCCGTCTCTCAAGAGT
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// cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
// cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
// cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
// cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
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// cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
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  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                     protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1752860 segs, 390397842 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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ORGANISM: Homo sapiens
US-10-371-942-118
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CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PLILNG DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-02-19
PRIOR PLILNG DATE: 2001-05-25
PRIOR PLILNG DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/270,349
PRIOR PLILNG DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/270,248
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1333
LENGTH: 253
                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1333
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US-10-293-418-1333
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                                                                                                                                           Sequence 118, Application US/10371942
| Publication No. US20030223994A1
| GENERAL INFORMATION:
| APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
| APPLICANT: Hoogenboom, Herricus Renerus Jacobus Mattheus
| TITLE OF INVENTION: MAC-PEPTIDE COMPLEX BINDING LIGANDS
| TITLE REPRENCE: 10280-034001
| CURRENT PILING DATE: 2003-02-20
| CURRENT FILING DATE: 2003-02-20
| PRIOR FILING DATE: 2002-02-20
| NUMBER OF SEQ ID NOS: 121
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 118
| LENGTH: 125
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Indels:
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25 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 42
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Mismatches:
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Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
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US-10-308-817-83
i Sequence 83, Application US/10308817
i Publication No. US20030219861A1
j GENERAL INFORMATION:
APPLICANT: Rother, Russell
j APPLICANT: Wu, Dayang
j TITLE OF INVENTION:
FILE REFERENCE: 1087-37
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SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 97
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; NUMBER OF SEQ ID NOS: 79; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 2
                                      LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2
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US-10-194-975-40
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Sequence 87, Application US/10032037B

Sequence 87, Application US/10032037B

Sequence 87, Application US/10032037B

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR PLICATION NUMBER: 60/258,948

FRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SEQ ID NOS: 204

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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 97
TYPE: PRT
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Sequence 87, Application US/1002998BB

Publication No. US20040001839A1

GENERAL INCORMATION:

APPLICANT: Bio-Technology General Corp.
                                                                                                                                                                                                                                                                    DELETED2 (1-81) x US-10-308-817-83 (1-97)
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US-10-308-817-83
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genence 83, Application US/10453698; Sequence 83, Application US/20040038308A1; GENERAL INFORMATION: APPLICATE ROCHET, RUSSell; TITLE OF INVENTION: HYBRID ANTIBODIES; FILE REFERENCE: 82 CIP (1087-37 CIP); CURRENT APPLICATION NUMBER: US/10/453,698; CURRENT FILING DATE: 2003-06-03; SOFTWARE: Patentin version 3.2; SOFTWARE: Patentin version 3.2; ERNGTH: 97
                                                                                                                                                                                                                                                                                                                                                              DELETED2 (1-81) x US-10-453-698-83 (1-97)
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US-10-029-926B-87
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CRGANISM: human
US-10-453-698-83
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Publication No. US20040002450A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: WIFTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE OF INVENTION: MORER: US/10/032,423A

CURRENT APPLICATION NUMBER: US/10/032,423A

CURRENT PILING DATE: 12/29/2000

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 97
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/209, 988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258, 948
NUMBER OF SEQ ID NOS: 204
SOPTWARE: FARLEQ for Windows Version 3.0
SEQ ID NO 87
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-032-423A-87
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Pred. No.:
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US-10-029-988B-87
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Mismatches:
Indels:

Gaps:

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Sequence 87, Application US/10029926B
Publication No. US20040073011A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILLS REFERENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 2001-12-31
PRIOR PILING DATE: 12/29/2000
NUMBER OF SELECTION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 203
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RESULT 10

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Best Local Similarity:
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Matches:
Conservative:
                   Sequence 47, Application US/10379392

Publication No. US20040110226A1

GENERAL INPORMATION:

APPLICANT: Lazar, Gregory Alan

APPLICANT: Desjarlais, John Rudolf

APPLICANT: Marshall, Shannon Allcia

APPLICANT: Dahiyat, Bassil I.

TITLE OF INVENTION: APTIBEDY OPTIMIZATION

FILE REFERENCE: A-71386-3 46307-236

CURRENT APPLICATION NUMBER: US/10/379,392

CURRENT FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 60/360,843

PRIOR FILING DATE: 2002-03-01

PRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PALENTIN VERSION 3.2

LENGTH: 97
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-733-532-128
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Pred. No.:
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Pred. No.:
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US-09-864-761-44315

US-09-864-761-44315

Sequence 4415, Application US/09864761

Fatent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wenbaheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: USEN EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-26

FRIOR FILING DATE: 2000-06-03
                                                                                                                                                                                                                                                       Sequence 12, Application US/10898408

Publication No. US20050058642A1

GENERAL INFORMATION:

APPLICANT: GALIBERT, Laurent J.

APPLICANT: YAN, Wei

ITLE REPERBYCE: 3467-A

CURRENT FILING DATE: 2004-07-23

FRIOR PILING DATE: 2004-07-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.2

LENGTH: 115
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US-10-898-408-12
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| PRIOR APPLICATION NUMBER: GB 24263.6|
| PRIOR FLIRE DATE: 2000.10.04|
| PRIOR PLINE DATE: 2000.10.04|
| PRIOR PLINE DATE: 2000.00.27|
| PRIOR PLINE DATE: 2000.00.27|
| PRIOR PLINE DATE: 2000.00.27|
| PRIOR PLINE DATE: 2001.01.30|
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DELETED2 (1-81) x US-09-864-761-44315 (1-117)

 Search completed: August 4, 2005, 20:23:29 Job time : 106.5 secs

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Sequence 716, App
Sequence 36503, A
Sequence 22691, A
Sequence 1333, Ap
Sequence 1333, Ap
Sequence 1333, Ap
Sequence 1333, Ap
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Sequence 122614,
Sequence 13695,
Sequence 2, Appli
Sequence 111396,
Sequence 130857,
Sequence 130896,
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Sequence 130969,
Sequence 151700,
Sequence 152186,
Sequence 40, Appl
Sequence 83, Appl
Sequence 77, Appl
Sequence 76, Appl
Sequence 69, Appl
Sequence 87, Appl
Sequence 87, Sequence 11363, Appl
Sequence 11363, Sequence 11367, A
Sequence 11363, Sequence 11367, Sequence 11367, Sequence 11367, Sequence 11367, Sequence 11367, Sequence 113631,
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Sequence 111128,
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Sequence 118, App
Sequence 110, App
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Sequence 111072,
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US-09-791-537-36503
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; Sequence 89288, Application US/09791537
; RENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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-D-fcgn2_1/USFV0_spool_1PNOLAN463-3B/runat_04082005_120455_19651/app_query.fasta_1.263
-DB=Pending_Patente_8_AA_Main_-QFMT=fastan_-SUFFIX=rapm_-MINMATCH=0.1_-LOOPCL=0
-LOOPEXT=0 -UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45_-DOCALIGN=200_-THR_SCORE=pot_TRM_AAL-100_-THR_MIN=0
-ALIGM=15
-MODE=LOCAL_-OUTFWT=pto_NORM=ext_-HEAPSIZE=500_-MINLEN=0 -ALIGM=15
-USER=NOLAN463-3B_GCGN_1 1_804_Grunat_04082005_120455_19651_-NCPU=6_-ICPU=3
-NO MANA_-LARCEGUERY_ARG_S=0_-MATRIX=DSPBLOCK=100_-LOORG_CG
-DEV__TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.1_-FGAPOP=6
-FGAPEXT=0.1_-YGAPOP=10_-YGAPEXT=0.1_-DELOP=6_-DELEXT=0.1_-FGAPOP=6
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Copyright (c) 1993 - 2005 Compugen Ltd

    protein search, using frame_plus_n2p model

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Xgapop 10.0 ,
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Database

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Sequence 144795, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER:
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER:
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION WUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARES: Patentin version 3.0
SOFTWARES: Patentin version 3.0
LENGTH: 97
LENGTH: 97
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Sedenbal INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debc, Derew
APPLICANT: Described to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 
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44 uProGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
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US-09-791-537-144795
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Best Local Similarity:
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US-09-791-537-111072
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SEQUENCE 11125, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: WOMBER: US/09/791,537
CURRENT APPLICATION UNMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 11128
                  APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 89288
LENGTH: 124
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13 LysLeuSerGluAspLeuSerLeuThrCysAlaValTyrGlyGlyGlySerPheSerGlyTyr 32
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; ORGANISM: Homo sapiens
US-09-791-537-111128
                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
  Debe, Derek
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US-09-791-537-89288
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Sequence 78283, Application US/09791537

Sequence 78283, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Dabe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE:
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE:
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE:
TITLE OF INVENTION: 151/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 78283
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: MOMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT RILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 22691
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13 LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
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ORGANISM: Homo sapiens
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; ORGANISM: HOMO E
US-09-791-537-78283
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SEQUENCE 36503. Application US/09791537

SEQUENCE 36503. APPLICANT: Bionomix, Inc.
APPLICANT: Bebe, Dereck
APPLICANT: Debe, Dereck
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
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TITLE OF INVENTION: METHODS OF USE THEREOF
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SCHENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOCTHARE: PATENTION OF USE THEREOF
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Sequence 716, Application US/09791537

Sequence 716, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bebe, Derek
APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFRENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUWBER OF SEQ ID NOS: 153055
SOCTWARE: Patentin version 3.0
SEQ ID NO 716
LENGTH: 119
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                                                                                                          49 yGlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65
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72.57%
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US-09-791-537-716
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US-09-791-537-36503
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US-09-791-537-36503
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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GENERAL INCORATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF52BCT
CURRENT APPLICATION NUMBER: PCT/USO1/19110
CURRENT PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1333
LENTH: 253
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Matches:
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PCT-USO2-36496-1333
; Sequence 1333, Application PC/TUSO236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
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PCT-US01-19110-1333
; Sequence 1333, Application PC/TUS0119110
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
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JOSEGUERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1333
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Matches:
Conservative:
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Indels:
FILE REFERENCE: PF523PCT2
CURRENT APPLICATION NUMBER: PCT/US02/36496
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1333
LENGTH: 253
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ORGANISM: Homo sapiens
US-09-880-748-1333
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ORGANISM: Homo sapiens
PCT-US02-36496-1333
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GENERAL INCUCRATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCES: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 00/331,469
FRIOR APPLICATION NUMBER: 60/331,469
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-12-19
FRIOR FILING DATE: 2001-12-19
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: 60/293,499
FRIOR FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: 60/297,379
FRIOR FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: 60/276,248
FRIOR APPLICATION NUMBER: 60/276,248
FRIOR APPLICATION NUMBER: 60/276,248
FRIOR APPLICATION NUMBER: 60/212,210
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-01-17
FRIOR FILING DATE: 2000-10-17
FRIOR FILING DATE: 2000-10-17
FRIOR FILING DATE: 2000-06-16
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US-09-791-537-110576
; Sequence 110576
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
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Query Match:
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64 sSer 65
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US-10-293-418-1333
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US-10-293-418-1333
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Pred. No.:
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DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBF DDS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 118, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al.
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034W01
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT APPLICATION NUMBER: US 60/358,994
; PRIOR PILING DATE: 2002-02-0
; NUMBER OF SEQ ID NOS: 121
; SSQTURAR: FELSEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THRRE DIMENSIONAL STRUCT
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNDMER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 110576
                                                                                                                                                                                                                                                                                                                                              DELETED2 (1-81) x US-09-791-537-110576 (1-121)
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US-09-791-537-110576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-05128-118
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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                                                                                                                                                           TYPE: PRT
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3 GGCGAGTCAGGATATTAGCAGC-----24
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Sequence 118, Application US/10371942
GENERAL INFORMATION:
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
APPLICANT: Reiter, Yoram
TITLE OF INVENTION: MAC-PEPTIDE COMPLEX BINDING LIGANDS
FILE REFERENCE: 10280-034001
CURRENT APPLICATION NUMBER: US/10/371,942
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,994
PRIOR APPLICATION NUMBER: US 60/358,994
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FESTESC for Windows Version 4.0
SEQ ID NO 118
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-371-942-118
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Conservative:
Mismatches:
Indels:
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Total number

Searched:

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Ig heavy chain V-IV region - human (fragment)

Ig heavy chain V-IV region - human (fragment)

C; Species: Homo eapleans (man)

C; Accession: B49028

R; Timmers: E.; Kenter, W. i. Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur. Bur. J. Immunod. 21, 2355-2363, 1991

A; Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob A; Reference number: A49028; MUID:92008140; PMID:1915549

A; Reference number: A49028

A; Residues preliminary

A; Molecule type: mRNA

A; Residues 1.143 orINA

A; Residues 1.143 orINA

A; Residues (B: S64473; NID:9236906; PIDN: AAB20012.1; PID:9236907

A; Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines

A; Note: sequence extracted from NCBI backbone (NCBIR:64473, NCBIP:64472)

C; Superfamily: immunoglobulin v region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin homology < IMM>

F; 15-97/ Domain: immunoglobulin homology < IMM>
Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig gamma chain V r Ig gamma chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r
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S26904
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I72667
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$31673
$24770
$19668
$26906
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    Percent Similarity:
Best Local Similarity:
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-WODEL=frame+ n2p.mcdel -DEV=xlp
-WODEL=frame+ n2p.mcdel -DEV=xlp
-WODEL=frame+ n2p.mcdel -DEV=xlp
-De-ford_1/USPTO_spool_p/NOLAN463-3B/runat_04082005_120454_19622/app_query.fasta_1.263
-DS-CALGR01_1/USPTO_spool_p/NOLAN463-3B/runat_0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=PIX -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNCTRAT=pto -TRR_SCORE=pct -THR_NAX=100 -THR_NIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=560 -MINIEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B_@CGN 1 1 63 @runat_04082005_120454_19622 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELDEXT=0.1
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                                                                                                August 4, 2005, 19:51:37 ; Search time 25 Seconds (without alignments) 623.485 Million cell updates/sec
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                                                                                                                                                                                    .....ACAACCCGTCTCTCAAGAGT
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(c) 1993 - 2005 Compugen Ltd
                                                                        protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
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S26805
S26806
S26806
S37454
JL0047
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S47010
S78055
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S78055
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1 CGGGCGAGTCAGGATATTAG.
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Database

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1011.6 1000.4 988.2 988.

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Result

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C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
Sptember 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A;Reference number: S37453
                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 S26806
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S26806
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
A;Reference number: S26806
A;Accession: $26806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-97/Domain: immunoglobulin homology < IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-106 <MCI>
A;Cross-references: BMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                           Percent Similarity:
Best Local Similarity:
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A; Residues: 1-97 < WEN>
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A; Status: preliminary
A; Molecule type: mRNA
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                                                                               Query Match:
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C, Species: Homo sapiens (man)
C, Species: Homo sapiens (man)
C, Species: Homo sapiens (man)
C, Date: 2.2-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C, Accession: S26898; 812420
J, Mol. 801. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Accession: S26885; MUID:93021117; PMID:1404388
A; Rocession: S26898
A; Molecule type: DNA
A; Residues: 1-97 < 470M>
A; Residues: 1-97 < 470M>
A; Residues: 1-97 < 470M>
A; Residues: 1-97 < 470M>
A; Residues: 1-97 < 470M>
A; Residues: 1-97 < 470M>
A; Residues: 209421; MUID:9005975; PMID:2511001
A; Accession: S12420
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Residues: 1-97 < 83N>
A; Residues: 1-97 < 83N>
A; Residues: 1-97 < 83N>
A; Residues: 1-97 < 83N>
A; Residues: 1-97 < 83N>
A; Residues: 1-97 < 83N>
A; Residues: 1-97 < 83N>
A; Cross-references: EMBL:X56364
A; Residues: 1-97 < 83N>
A; Cross-references: EMBL:X563001 imunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 15-97/Domain: immunoglobulin homology < 1MM>
F; 15-97/Domain: immunoglobulin homology < 1MM>
A; Residues: 1-97 < 100 A; Reymords: heterotetramer; immunoglobulin F; 15-97/Domain: immunoglobulin A; Residues: heterotetramer; Remannoglobulin A; Residues: heterotetramer; Remannoglobulin A; Residues: heterotetramer; Remannoglobulin A; Residues: heterotetramer; Remannoglobulin B; R
                RESULT 2
S26805
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
A;Reference number: 5268005 #UID:92201299; PMID:1348029
A;Accession: S268005
A;Accession: S268005
A;Accession: S268005
A;Accession: S268005
A;Accession: S268005
A;Crose-reference: EMBL:Z1421; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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13 LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
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Conservative:
Mismatches:
Indels:
Gaps:
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37.74%
71.71%
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Pred. No.:
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DB:
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Alignment Scores: 0.00023 Length: 126  Score: 98.20 Matches: 19 Score: 98.20 Matches: 19 Percent Similarity: 65.62% Conservative: 2 Best Local Similarity: 59.38% Mismatches: 3 Query Match: 2 Query Match: 2 Gaps: 0  CCAACT 61 DELETED2 (1-81) x 847010 (1-126)		RESULT 8 S78052 Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man) C;Species: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78052; S23717 R;Harindranath, N. Submitted to the EMBL Data Library, August 1990 A;Reference number: S78051 A;Accession: S78052	stop codon; the se	A, Accession: 523715, MUID:92031262; PMID:1718404 A, Accession: 523717 A, Molecule type: mRNA A, Residues: 15-111 <haw> A, Cross-references: EMBL:X54441 C, Superfamily: immunoglobulin V region; immunoglobulin homology C, Reywords: immunoglobulin F;1-14/Domain: signal sequence (fragment) #status predicted <sig>F;15-140/Product: 1g heavy Chain (fragment) #status predicted <mat>F;29-111/Domain: immunoglobulin homology <imm></imm></mat></sig></haw>		23-Jul-1999  Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCATAGTGGAAGCACCAACT Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCATAGTGGAAGCACCAACT	RESULT 9 A49045 Ig heavy chain V region (anti-B cell autoantibody) - human (fragment) C;Species: Homo sapiens (man) C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999 C;Accession: A49045 R;Grillot-Courvalin, C.; Brouet, D.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silver, J. Immunol. 22, 1781-1788, 1992 Bir. J. Immunol. 22, 1781-1788, 1992 A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes
Score: 98.20 Matches: 19   Percent Similarity: 65.624 Conservative: 2   Best Local Similarity: 59.384 Mismatches: 3   Query Match: 70.144 Indels: 8   Best Local Similarity: 59.384 Mismatches: 3   Dels: 8   Dels: 8   Dels: 8   Dels: 8   Dels: 9   Db 20 GlyLysGlyLeuGluTrpileGlyGlulleAsnHisSerGlySerThrAsnT Oy 62 ACAACCGTCTCTCAAGAGT 81	JL0047  JL0047  Jg heavy chain V region precursor (clone cR18) - human  Jg heavy chain V region precursor (clone cR18) - human  C; Species: Homo sapiens (man)  C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-  C; Accession: JL0047  R; Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.  J. Exp. Med. 167, 2011-2016, 1988  A; Title: Immunoglobulin V-H genes are transcribed by T cells in ass A; Reference number: JL0047; MUID:88258392; PMID:3133445  A; Molecule type: mRNA	estdues: 1-122 ABAE> xperimental gource: T-cell line RPMI 8402 ote: the authors translated the reading frame which extends to the ote: this acquence belongs to the VH II subgroup perfamility: immunoglobulin V region; immunoglobulin homology eywords: heterotetramer; immunoglobulin homology 3-105/Domain: immunoglobulin homology <imm></imm>	Alignment Scores: 0.00023 Length: 122 Score: 98.20 Marches: 19 Percent Similarity: 65.62\$ Conservative: 2 Best Local Similarity: 59.38\$ Mismatches: 3 Query Match: 2 DB: 2 Gaps: 0 DELETED2 (1-81) x JL0047 (1-122)	2 GGGCGAGTCAGGATATTAGCAGCTGCTTAGCCGAAATCAATC	RESULT 7 847010 19 heavy chain V4.21-UniqueD-J5 region - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Accession: 847010 R.Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Caisubmitted to the EMBL Data Library, July 1994 A.Description: The role of the immunoglobulin heavy chain in human	A; Accession: 847009 A; Accession: 847010 A; Accession: 847010 A; Accession: 847010 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-126 Aman: A; Residues: 1-126 Aman: 235492; NID:g517254; PIDN:CAA84625.1; PID:g517255 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 15-97/Domain: immunoglobulin homology < IMM>	

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C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
Li, Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap. A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)
C;Species: Home sapiens (man)
C;Date: 22-Nov-1993 Heequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826905; 812419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty A;Reference number: $26885; MuID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||::: ||| ClyLeu----GluTrplleGlyGluIleAsnHisSerGlyGlyThrAsnT
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|Trp1leGlyGlu1leAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCGGTCTCTCAAGAGT
                                     A,Molecule type: mRNA
A;Residues: 1-133 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;9-38/Region: framework 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIRROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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     A; Reference number: PS0341; MUID: 92171937; PMID: 1540170
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Gaps:
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94.20
62.50%
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70.00%
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                         A;Accession: PS0341
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1923746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
N;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
N;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglangerence number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23746
A;Accession: B23746
A;Accession: Drotein
A;Residues: 1-231 <-LEO
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Ig heavy chain V-D-J region (RAMOS) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997

C;Accession: PS0341

R;Ratech, H.

Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992

A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
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A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-140 cGRI>
A;Cross-references: GB:S39381; NID:9250899; PIDN:AAB22441.1; PID:9250900
A;Cross-references: GB:S39381; NID:9250909; PIDN:AAB22441.1; PID:9250900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keyworfa: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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F;140-209/Domain: immunoglobulin homology <1MM>
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59.38%
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Search completed: August 4, 2005, 20:05:40 Job time: 27 secs
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           48.89%
46.67%
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uLysSer 83
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Best Local Similarity:
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-97 < ESJ>
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A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Orce: designated DP-70
R;Sarz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:Z511001
A;Accession: S12419
A;Scatus: preliminary; translation not shown
A;Accession: S12419
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment)
C;Species: Homo sapiens (man)
R;Harindranath, N.
R;Harindranath, N.
R;Harindranath, N.
R;Molecule type: mRNA
A;Residues: 1-145 < HAR>
A;Residues: 1-145 < HAR>
A;Coross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GlyGlySer----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy 44
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A; Residues: 18-115 < HAW>
A; Residues: 18-115 < HAW>
A; Cross-references: EMBL:X54445
A; Note: the authors translated the codon GCA for residue 67 as Arg C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
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R; van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
                                                                                                                                               43 GlyGlySer----ileSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-97/Domain: immunoglobulin homology < IMM>
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TISSUE-HOGGKIN lymphoma;

Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,

Tinguely M.L., Brauninger A.;

Submitted (MAY-2013) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ564425; CAD92032.1; -.

HSSP; P18532; IKCV.

InterPro; IPR00110; Ig-like.

InterPro; IPR003596; Ig-V.

SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rearranged VH4-34 V gene segment (Fragment)
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                                                 Q72379
HV47 MOUSE
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Q6TJQ4
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Q810632
Q61LBQ5
HV46 MOUSE
Q7ZBB2
Q90QT5
Q9QKY2
Q698Z8
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096xx8
060J60
060J62
099CH3
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09IUP1
09IUR6
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Q9IUQ5
Q9J783
Q9IUT6
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 Q9UL73
Q6GMX1
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                             - protein search, using frame plus n2p model
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Q6GABZ 2
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Q99M22
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HV61 MOUSE
Q65XII
HV61 MOUSE
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Listing first 45 summaries
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: uniprot_sprot:*
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Straubberg R.L., Feingold E.A., Grouse L.H., Darge J.G.,

Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tocahiyuki S., Carninci P., Prange C.,

Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesbey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

and mouse Anna certain and limital analysis of more than 15,000 full-length human
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Straubberg R.;
Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.2; -.
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
PFRan; PP07654; C1-set; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00239; IG LIKE; 5.
PROSITE; PS00239; IG LMEC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 il protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
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Last sequence update)
Last annotation update)
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Mismatches:
Indels:
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Matches:
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                                                                    01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. Homo sapiens (Human).
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                            42
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TISSUB-Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETURE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETURE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RIJAUSHORF R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raphan R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninori P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.R., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A lones S.J., Marra M.A.;

and mouse C.DNA sequences.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073767; AAH73767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 65304 MW; 2A1E75F6AED85230 CRC64;
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                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                      597 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                      PRT;
81
                        InterPro; IPR003599; IG.
InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF007654; C1-set; 4.
Pfam; PF0047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
62 ACAACCCGTCTCTCAAGAGT
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65.62%
59.38%
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                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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DELETED2 (1-81) x Q96AA6 (1-625)
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shaefer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antschul S. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Antidon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garrica A.M., Gay L.J., Hulyk S.W.,
Antidon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Radesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
Ander S.J., Marra M.A.,
Ander S.J., Marra M.A.,
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Ander S.J., Marra M.A.,
Ander S.J., Marra M.A.,
Ander S.J., Marra M.J.,
Ander S.J., Marra M.A.,
Ander S.J., Marra M.J.,
Ander S.J., Marra M.J., Marra M.
                                              78
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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SMART; SM00406; IGV: 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SEQUENCE S97 AA; 65274 MW; 2DAFARBTE055851 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Conservative:
Mismatches:
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Gaps:
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                                                                                                                   62 ACAACCCGTCTCTCAAGAGT 81
                                                                                                                                                          nasc, ress, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequences
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGHM protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                              61
                                                                                                                                                                                     78
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                                                                                                                                                                                                                                                                                                                                       Q9BU10
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9
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**X TASUSELYMPROPE;

**X MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

**A Klausher R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

**A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.P., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.P., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.P., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.P., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.P., Bhat N.K.,

**A Altschul S.F., Zeeberg B. B. Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Robard S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**A Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Niting M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A Nhiting M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A Richards M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**A Jones S.J., Marra M.A.,

**Jones S.J., Marra M.A.,

**A Jones S.J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg'R';
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017355; AAH17356.2; -.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 625 AA; 68610 MW; P62FAB3ADE7ECBFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625
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                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                 625 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                 PRT;
   81
                                                               84
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InterPro; IPR00110; Ig-11ke.
InterPro; IPR00110; Ig-21.
InterPro; IPR001359; Ig_C1.
InterPro; IPR0013596; Ig_WHC.
InterPro; IPR001596; Ig_W-
Pfam; PR07654; C1-8et; 4.
SMART; SM00407; IG2; 4.
SMART; SM00407; IGC1; 4.
01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.000541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.20
65.62%
59.38%
70.14%
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             IGHM protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                          RESULT 5
Q96AA6
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ACAACCCGTCTCTCAAGAGT

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                                                                                                     Q6P418;
                                                                                         06P4I8
                                                                RESULT 7
                                                                             Q6P4I8
                                                                                                     셤
                                                                                                                                                                                                                                                                MEDLINE=2218825; PubWed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2218825; PubWed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 GlyLys----GlyLeu----GluTrplleGlyGlulleAsnHisSerGlySerThrAsnT 85
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALCAL, PEO7654; L. SMART; SM00406; IGv; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; S. PROSITE; PS00290; IG MHC; UNKNOWN 3. PASITE; PS00290; IG MHC; UNKNOWN 3. PASITE; PS00290; IG MHC; UNKNOWN 3. PASITE; PS00290; IG MH; 2DAFADS0A6375851 CRC64; PS07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
128
14
18
19
                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
IGHM procesin.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                  597 AA
                                                                                                                 PRT;
                                       81
                                                    HSSP; P01861; 1ADQ.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR0031597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 4.
                                       ACAACCCGTCTCTCAAGAGT
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62.50%
56.25%
65.86%
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                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                       62
                                                                                                                              298088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                  98086C
                                                                                      RESULT 6
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TISSUE=Primary B-Cells;

WEDINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KIAUSE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RIAUSERT R.D., Collins F.S., Magner L.D., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

An Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.D., Dickson M.G.,

Raha S., Worley A., Stockergren E.D., Dickson M.G.,

Raha S., Marra M.A., Youchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. And mouse CDNA sequences: ",

                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBB97C949D720F1E CRC64;
                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
   576 AA
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PROSITE; PS00290; IG MHC; UNKNOWN
SEQUENCE 576 AA; 63363 MW; FBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; IG.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003066; Ig-MHC.
InterPro; IPR003066; Ig-WHC.
InterPro; IPR003596; Ig-v.
Pfam; PF007654; C1-8et; Z.
SMART; SM00409; IG; 1.
SMART; SM004009; IG; 1.
SMART; SM004007; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.00377
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48.89%
46.67%
65.71%
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                   GHD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                         Name=IGHD;
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DELETED2 (1-81) x Q6P4I8 (1-576)

deleted2.rup

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                52 GlyGlySer----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy
                                                          -----TGGTTAGCCGAAATCAAATCATAGTGGAAGCACCAACTACAACCCGTCTCT
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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J segment.
J segment.
By similarity.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human)
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GGCGAGTCAGGATATTAGCAGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1. 2—NARRT; SM00406; IGV; 1. PROSITE; PS56835; IG LIKE; 1. Immunoglobulin V region; Signal.
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Best Local Similarity:
                                                                                                                       CAAGAGT
                                                                                                                                                                                                              HV2I HUMAN
P06331;
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Q6GMX7;
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DOMAIN
DOMAIN
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1D HV21_H

DT 10-JAN1,

DT 10-JAN1,

DE 15-JUL-

DE 15-JUL-

DE 19 hear 1,

OX NCB1_T

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TISSUE=Primary B.CEL18;

KR Strausberg R.D., Febingold B.A., Grouse L.H., Derge J.G.,

KRausberg R.D., Febingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschako L., Marusina K., Farer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

Raplacon M., Soares G.J., Abramson R.D., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gub S., R.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,

Richards A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marza M.A.; RA, S., A., Myers R.M., Butterfield Y.S.,

Rapparish M.J., Salska U., Smailus D.E., Schnerch A., Schein J.E.,

Rapparish M.J., Shalska U., Smailus Of more than 15,000 full-length human more colly sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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| GlyGlySer----IleSerSerTyrTyrTrpSerTrp1leArgGlnThrAlaGlyLy8Gl
05-JUL-2004 (TEMBLrel. 27, Created)
05-JUL-2004 (TEMBLrel. 27, Last sequence update)
05-JUL-2004 (TEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical Melacona (Creation of the Spiens (Human).
Eukaryota; Melacona (Creation Creation):
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Conservative:
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Indels:
Gaps:
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Pfam; PF00047; ig; 3.
SNART; SM00409; IG; 4.
SNART; SM00406; IG; 13.
SNART; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990A1
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77.10
45.45%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GlyGlySer----ileSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 -----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTAA
                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone_CSODL004YM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGHM protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                Homo sapiens (human) (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUEs-primary B-Cells;
MEDILNE=22388257, Pubmed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IRR005596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                             Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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79.10
47.73
43.18
56.50
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                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=B cells;
                                                                                                                                                                                                                                                                                                                                             rISSUE=B cells;
i W.B., Gruber C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sser 97
84
                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                              086SX2
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006EY0
DT 01-DE
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley.K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raheton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukarwota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extransberg R.;
Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857, A4H11857.2;
R PIR; S15590; S15590.
R HSPS; PO1820; 1G70.
R InterPro; IPR001599; Ig.
R InterPro; IPR00110; Ig-like.
R InterPro; IPR001309; Ig_MHC.
R InterPro; IPR001306; Ig_MHC.
R InterPro; IPR001306; Ig_MHC.
R InterPro; IPR001306; Ig_WHC.
R SMART; SM00409; IGG.2.
R SMART; SM00400; IGG.1; 4.
R SMART; SM00406; IGG.1; 4.
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119
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Conservative:
Mismatches:
Indels:
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                                                                MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
A strachul S.F., Zeeberg B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A pitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wackernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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31 LysProSerGlnSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN 2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC002091; AAH02091.1; -.

HSSP; P018020; 1G7J.

InterPro; IPR00110; Ig-11ke.

InterPro; IPR003109; Ig_C1.

InterPro; IPR003597; Ig_C1.

InterPro; IPR003595; Ig_MHC.

InterPro; IPR003595; Ig_MHC.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR004055; Ig_MHC.

InterPro; IPR004055; Ig_MHC.

InterPro; IPR004055; Ig_MHC; IGPNCNONN_2.
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479 AA; 51992 MW; 768E39A138918892 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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HV61 MOUSE
D HV61 MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV (Rel. 45, Last annotation update)
DF 25-OCT--2004 (Rel. 45, Last annotation update)
DF 19 heavy chain V region 1843 precursor.
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STRALN-mix FVB/N; TISSUE-Mammary tumor;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBan
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37.04%
27.78%
54.50%
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Query Match:
                                              SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA
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SEQUENCE 47
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Pred. No.:
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-----AGCTGGTTAGC 32
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                                                                                           STRAIN=BALB/cJ;
MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
                Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                         primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-I- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 yTyrlleHisTyrSerGlyAsnThrSerTyrAsnProSerLeuLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 CGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region 1B43.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13158 MW; 1CB547253681FF74 CRC64;
                                                                                                                                                                                                      PIR; JT0508; HVMSIB.
PDB; 1KCS; X-ray; H=19-116.
PDB; 1KCY, X-ray; H=19-116.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
Fram; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
PROSTIE; PS50835; IG_LKE; 1.
PROSTIE; PS50835; IG_LKE; 1.
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(TrEMBLrel. 27, Last sequence update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                       Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELETED2 (1-81) x HV61_MOUSE (1-116)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.517
75.70
56.76%
43.24%
54.07%
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                                                                                                                                                                                                                                                                                                                                                                                     48
53
67
84
116
                                                                                SEQUENCE FROM N.A.
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Best Local Similarity:
                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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05-JUL-2004
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DISULFID
STRAND
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SEQUENCE
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ID Q6GMX6
AC Q6GMX6;
                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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DB:
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178 SerGlyTyr-TrpAsnTrp1leArgLysPheProGlyAsnLysLeuAspTyrMetGlyTy 197
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                                                                                                      TISSUB-Primary B-Cells,

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klauberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K.A., Farmer A.A., Rubin G.M., Hong L.,

A Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH7766.1; -...
InterPro; IPR003599; Ig.-..
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_W.-.
InterPro; IPR003596; Ig_W.-.
InterPro; IPR003596; Ig_W.-.
Efam; PF0047; ig; 4.
SWART; SM00409; IG; 2.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
116
2
6
6
0
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
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Indels:
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75.20
56.25%
50.00%
53.71%
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
              Hypothetical protein. Homo sapiens (Human).
                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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Q65211;
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DB:
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Q65ZII
ID Q65ZI
AC Q65ZI
 8
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9 TCAGGATATTAGCAGCTGGTTAGCCGAA------

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Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
"Targeting human immunodeficiency virus type 1 reverse transcriptase
IT by intracellular expression of single-chain variable fragments to
inhibit early stages of the viral life cycle.";
J. Virol. 70:3392-3400(1996).

REMBL; U48716; AAB64342.1; -.
RO, GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
InterPro; IPR003599; IG-2.
REMINITY SM00409; IG-2.
REMINITY SM00409; IG; 2.
REMART; SM00409; IG; 2.
REMART; SM00409; IGC2; 2.
REMART; SM00406; IGV; 2.
                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
Bukarvete (Mouse)
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16
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112
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                             TISSUE=Hybridoma;
MEDLINE=96211469; PubMed=8648670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-directed DNA polymerase.
SEQUENCE 262 AA; 27842 MW;
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72.80
55.56%
44.44%
52.00%
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Best Local Similarity:
                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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